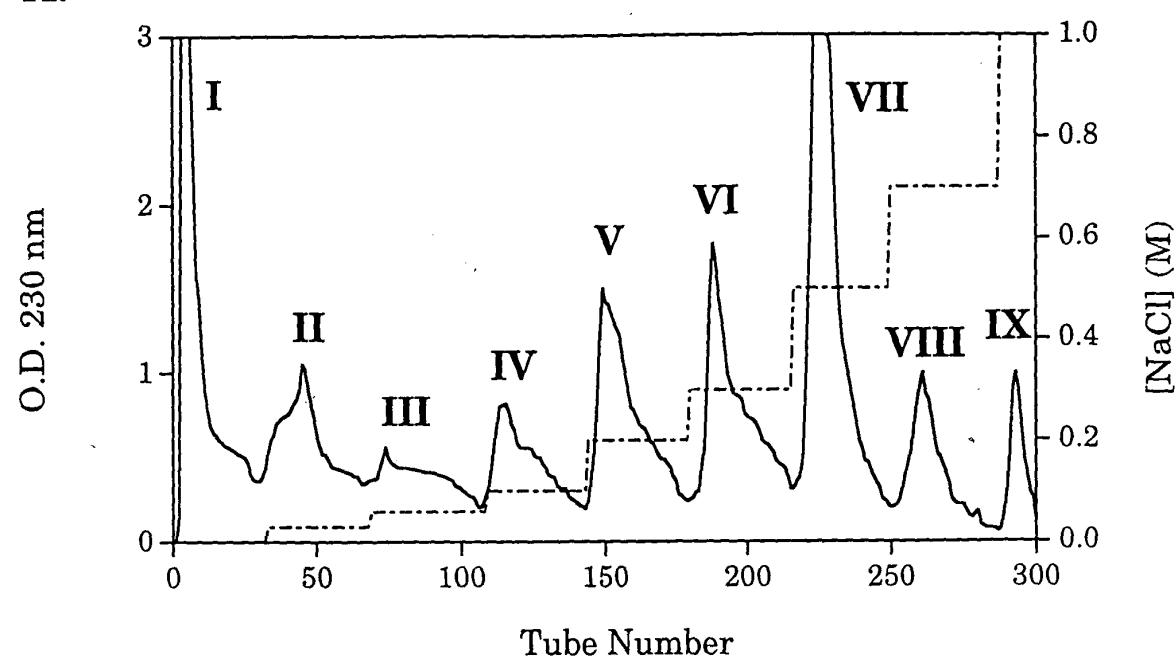


FIG 1.0

A.



B.

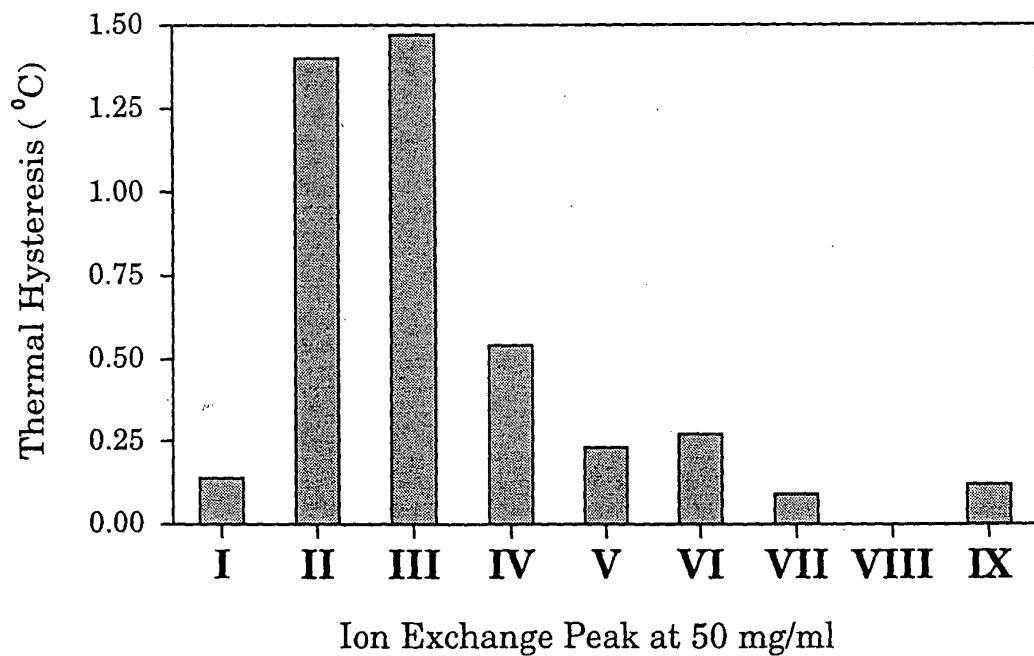


FIG 1.1

FIGURE 1.2. GEL ELECTROPHORESIS

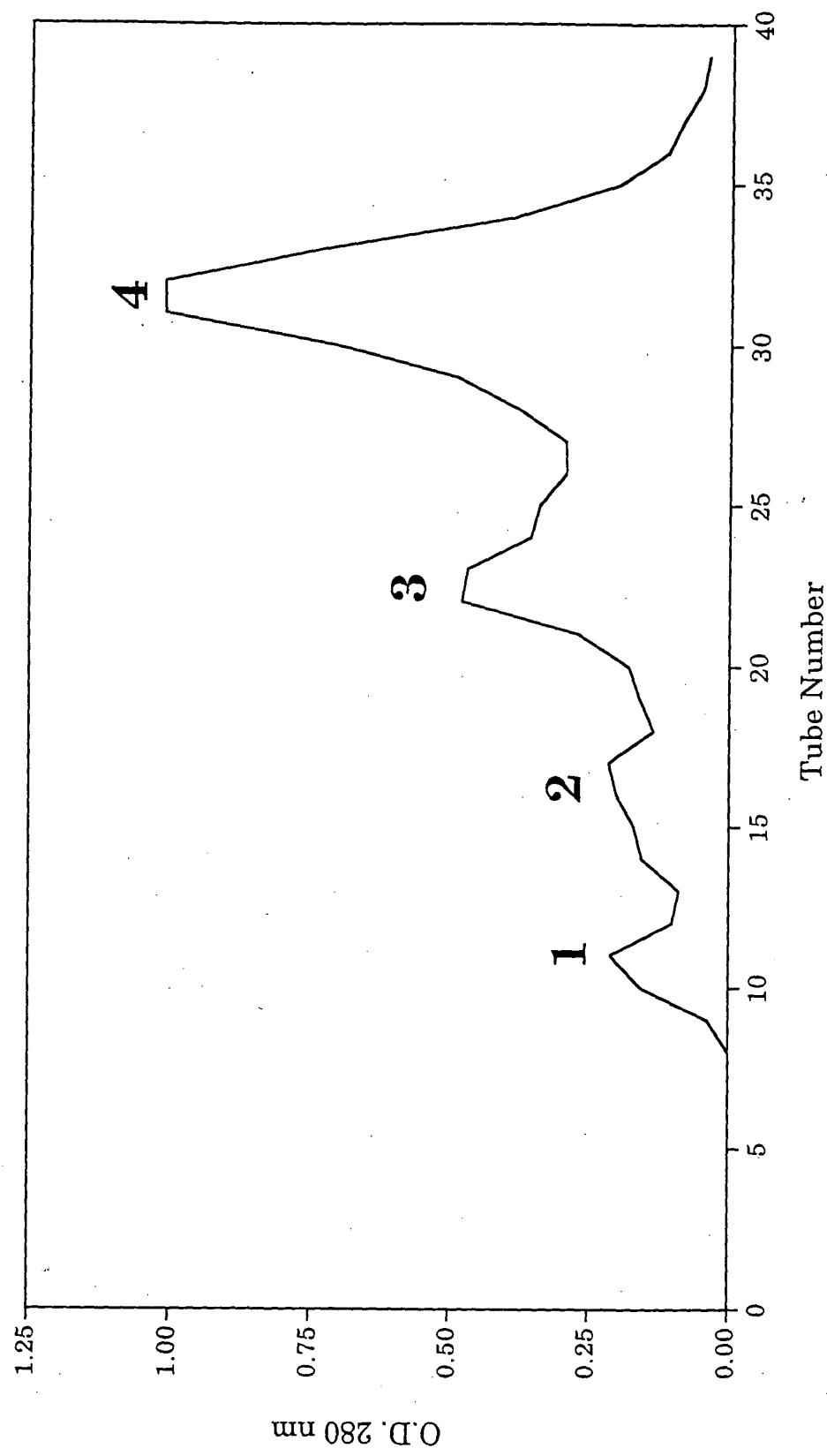


FIG. 1.2

0 9 8 7 6 5 4 3 2 1 0



FIG 1.3

Tm-12.86►

12.5 25

FIG 1.4

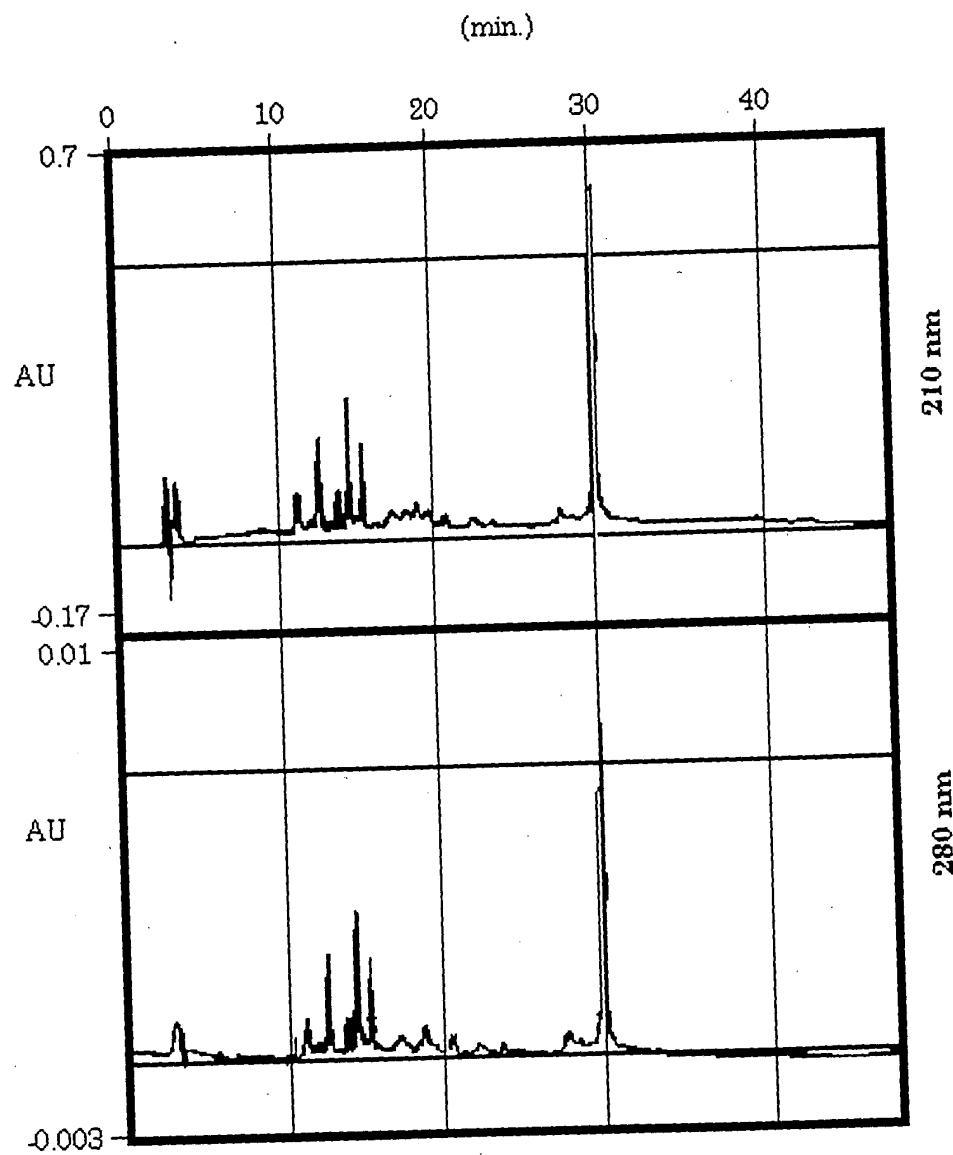


FIG 1.5

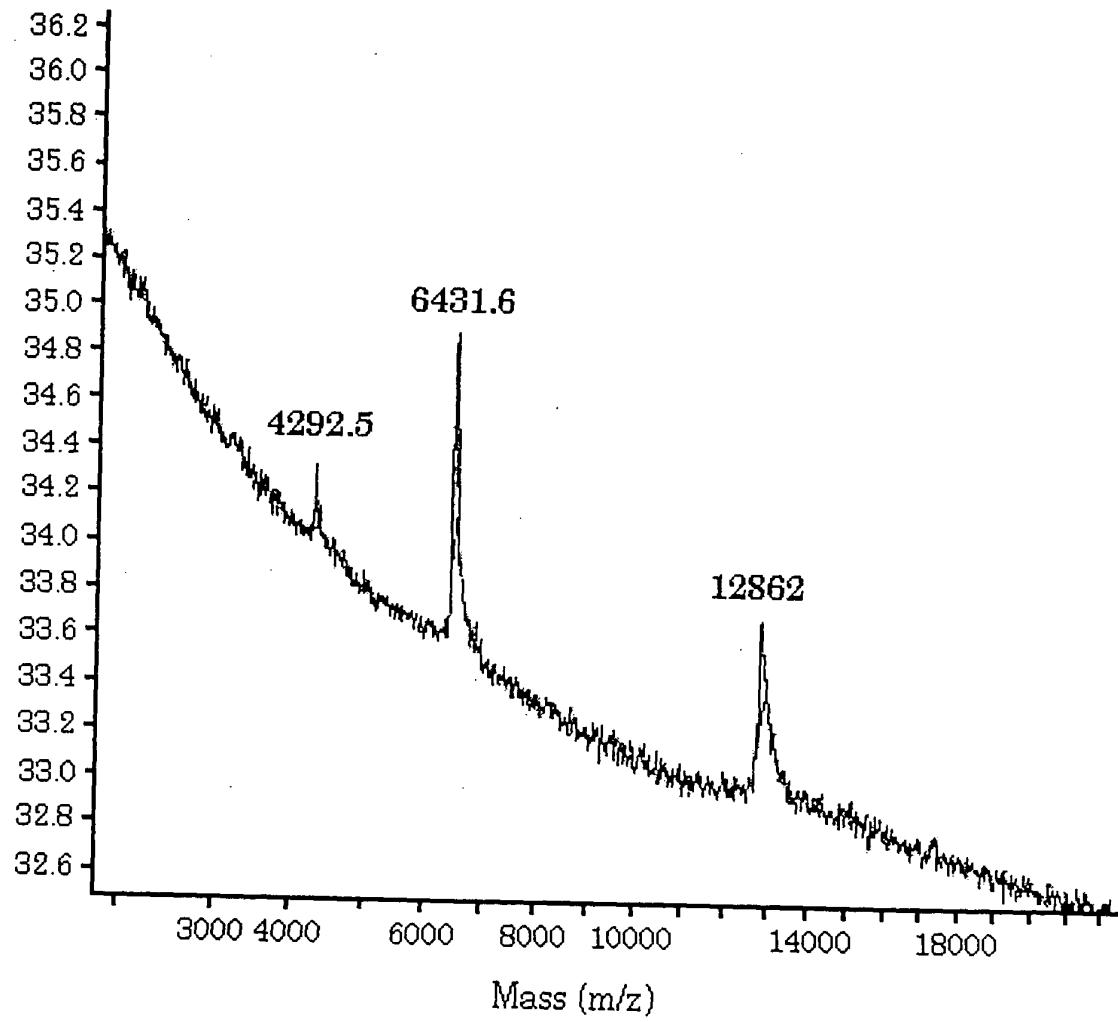


FIG 1.6

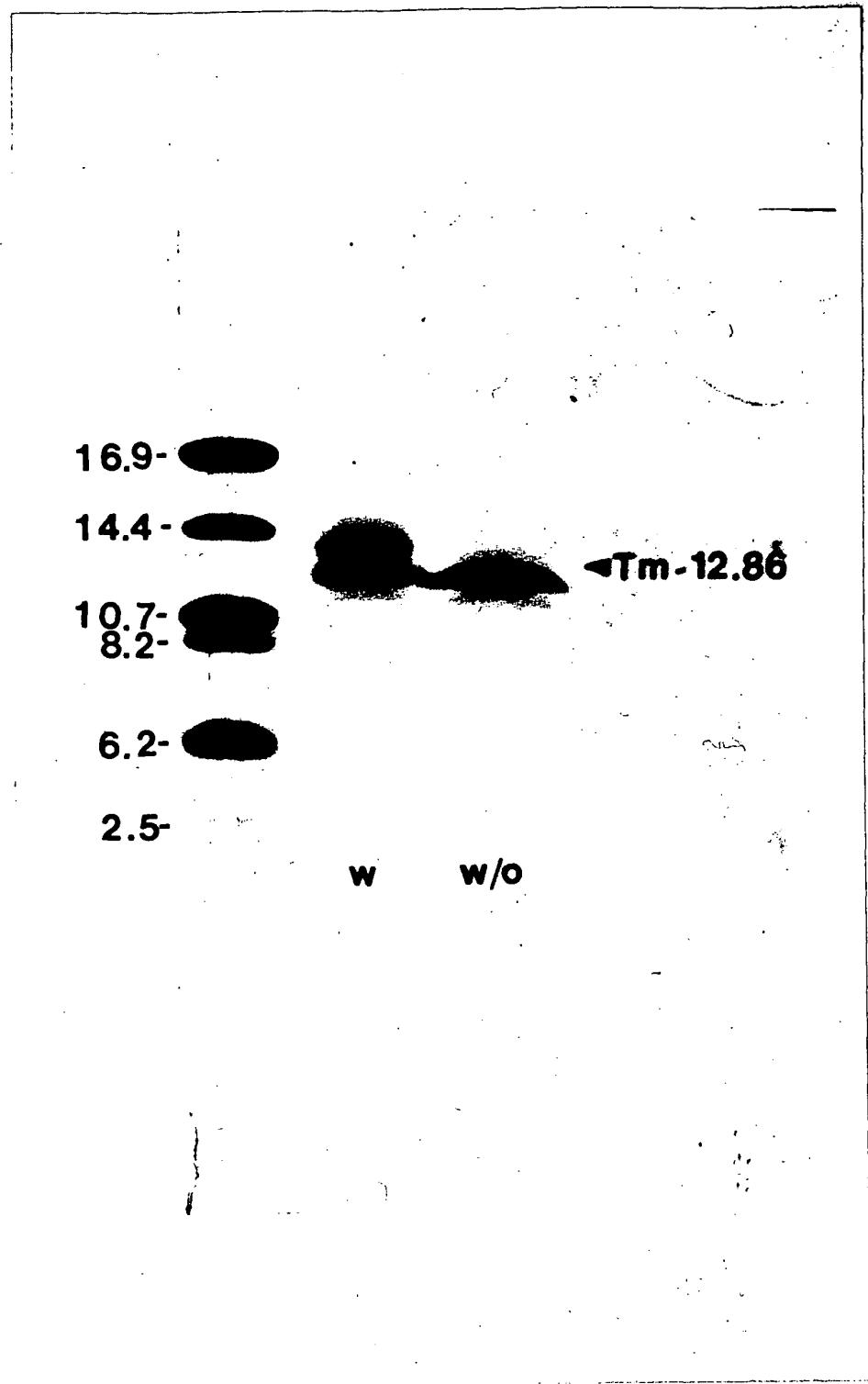


FIG. 1.7

NH₂-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?Q-Q-V

Leu	Thr	Asp	Glu	Gln	Ile	Lys	Arg	Asn	Ile	Lys	Ser	Ile	Lys	Glu	Gln	Gln	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

FIG. 1.8

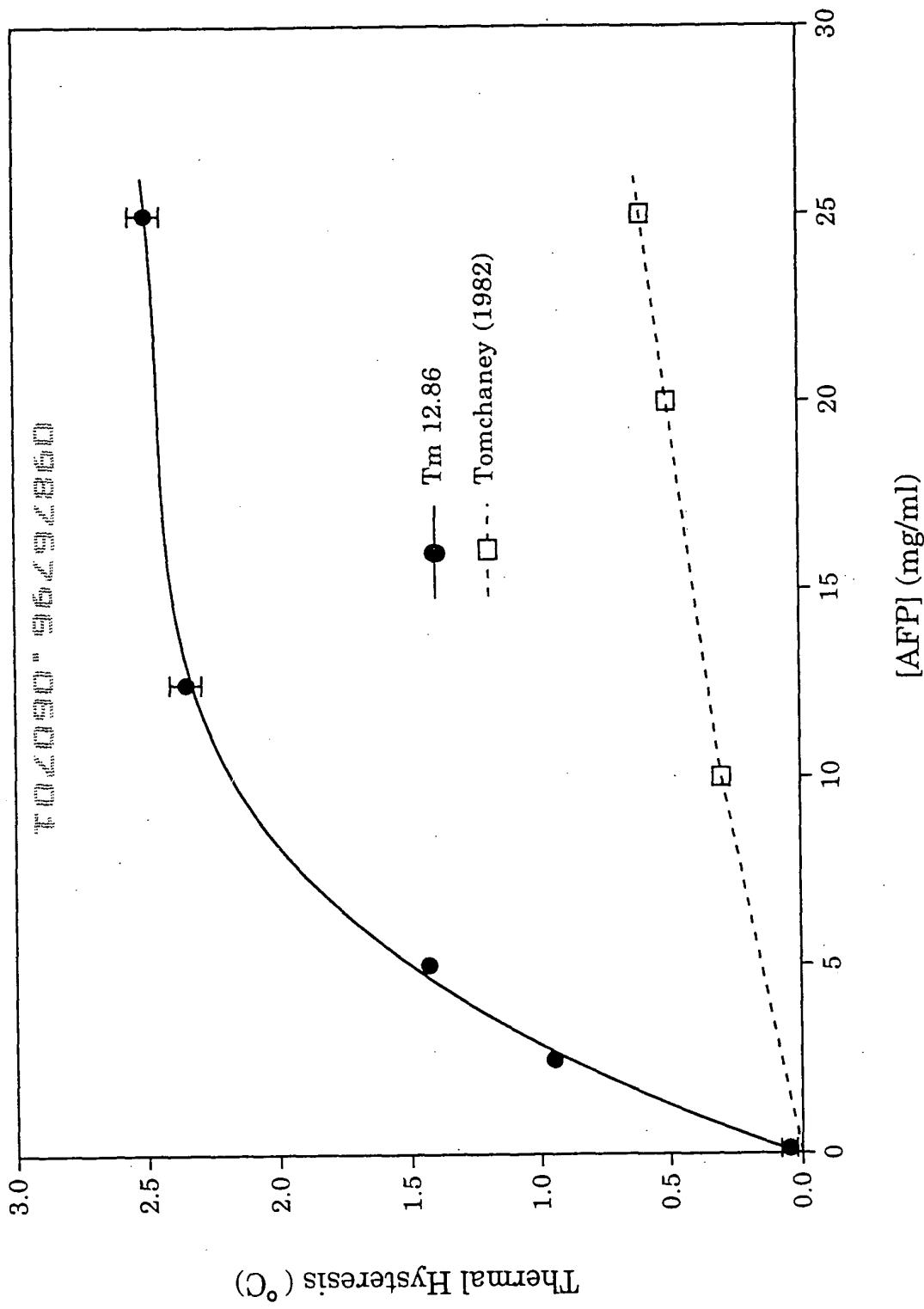


FIG 1.9

09376796 - 060204

1 2.5 5 10 15 20 H

-44.0

-32.3

-17.4

-7.8

FIG 1.10

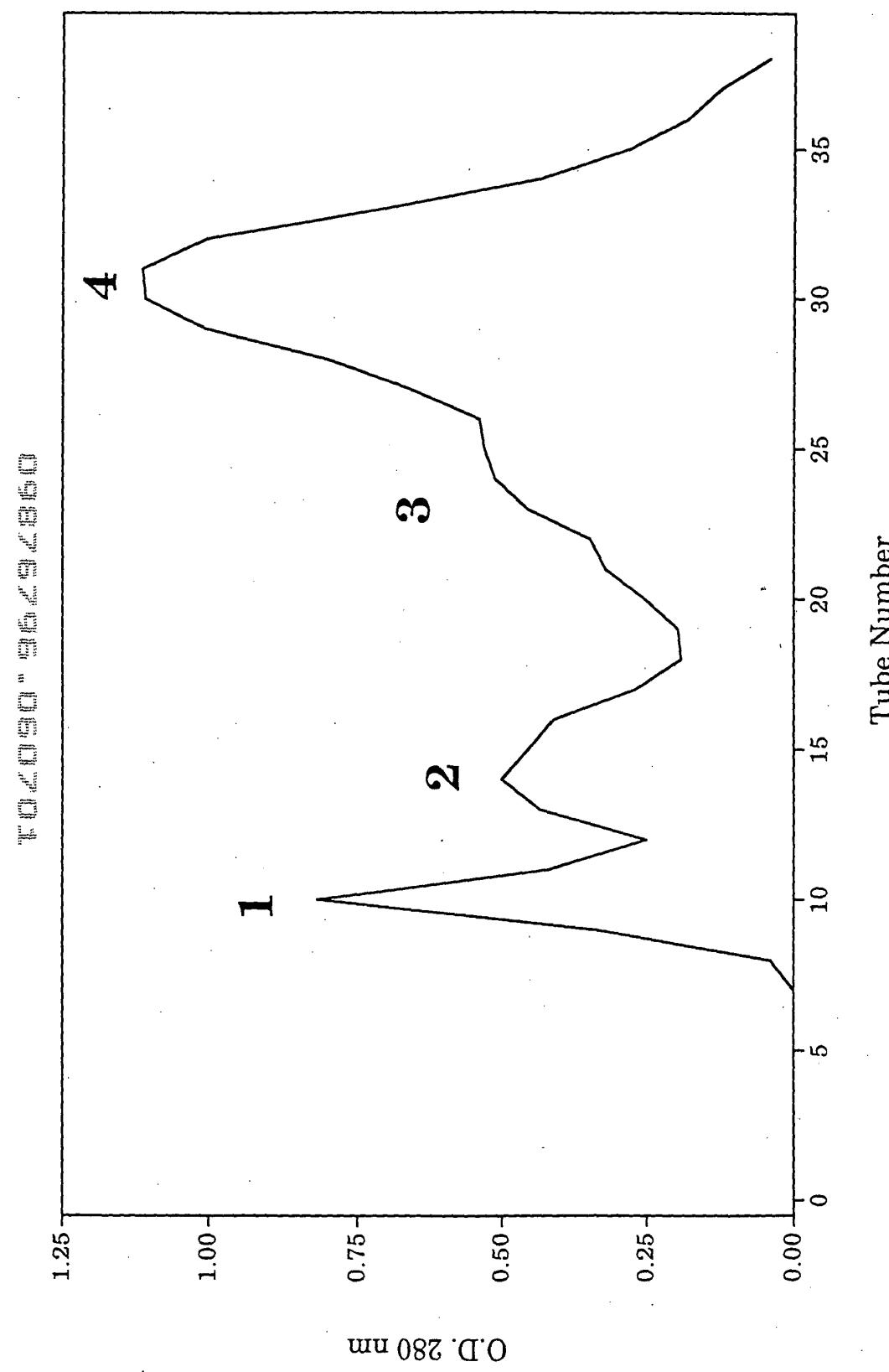


FIG 1.11

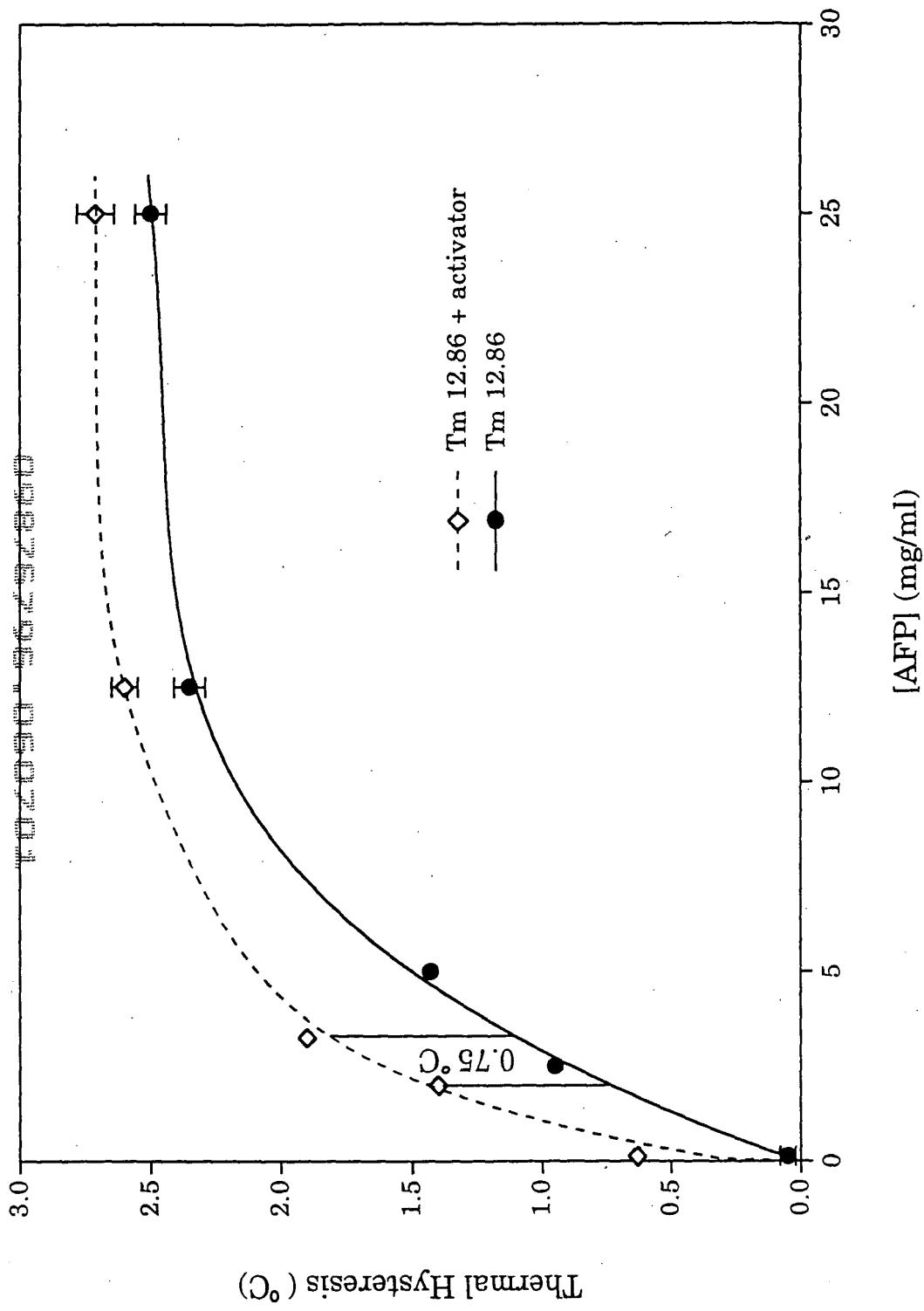


FIG 1.12

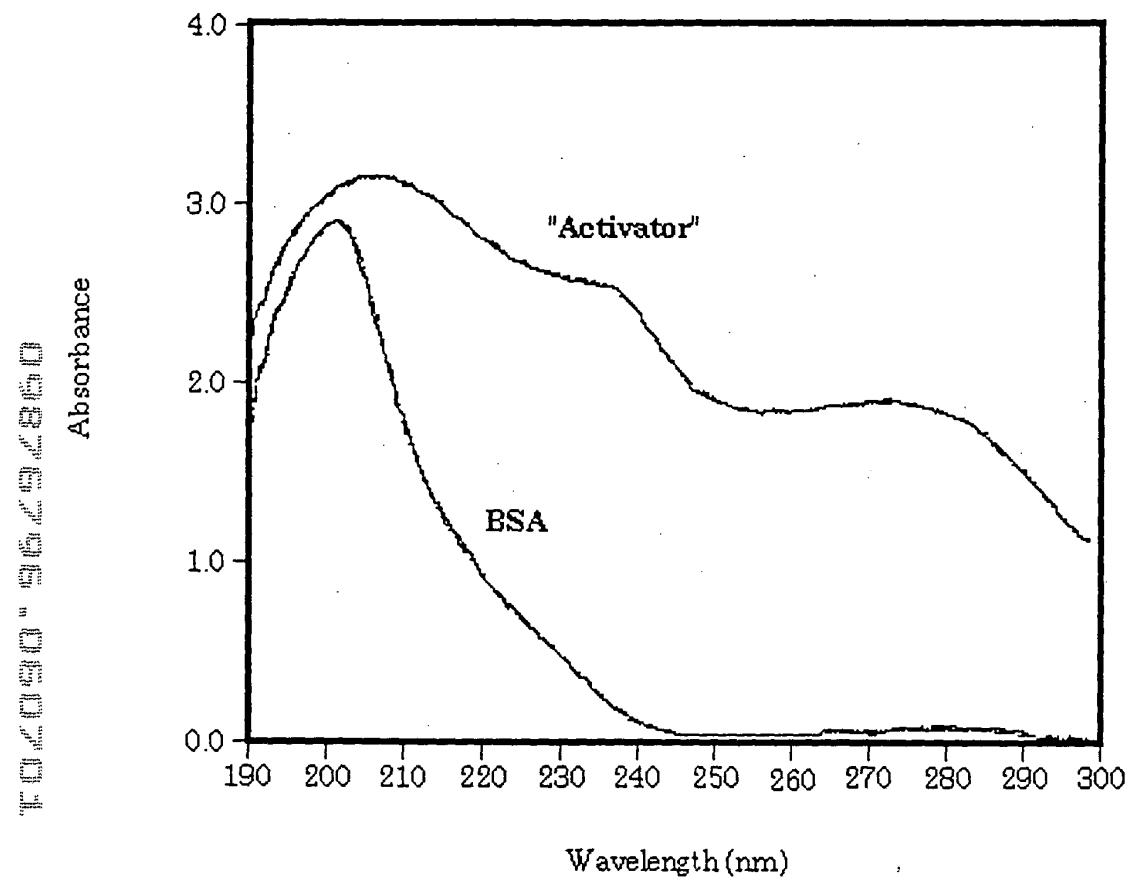


FIG 1.13

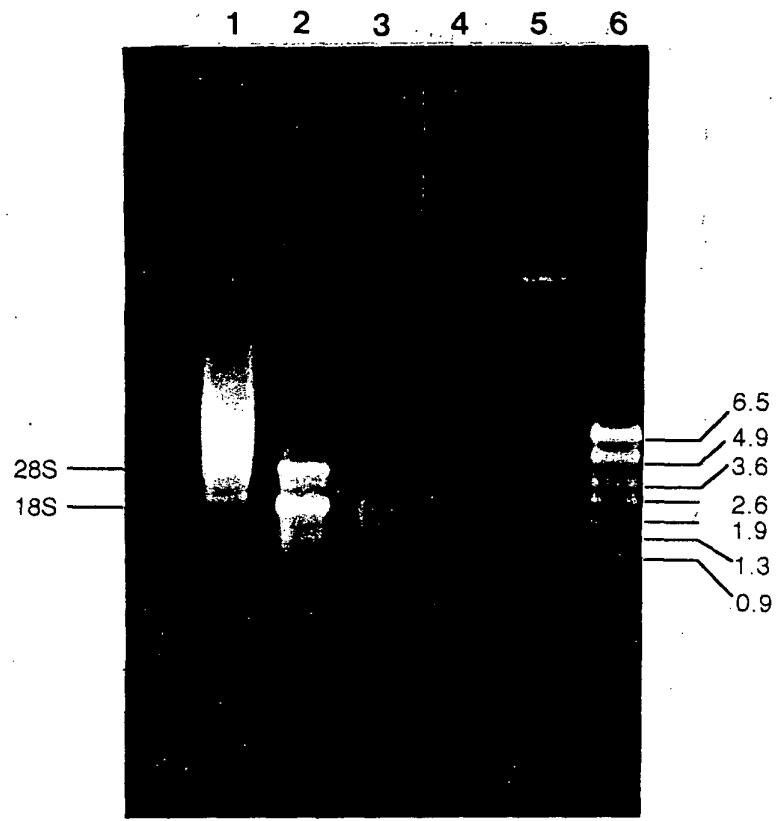


FIG 2.0

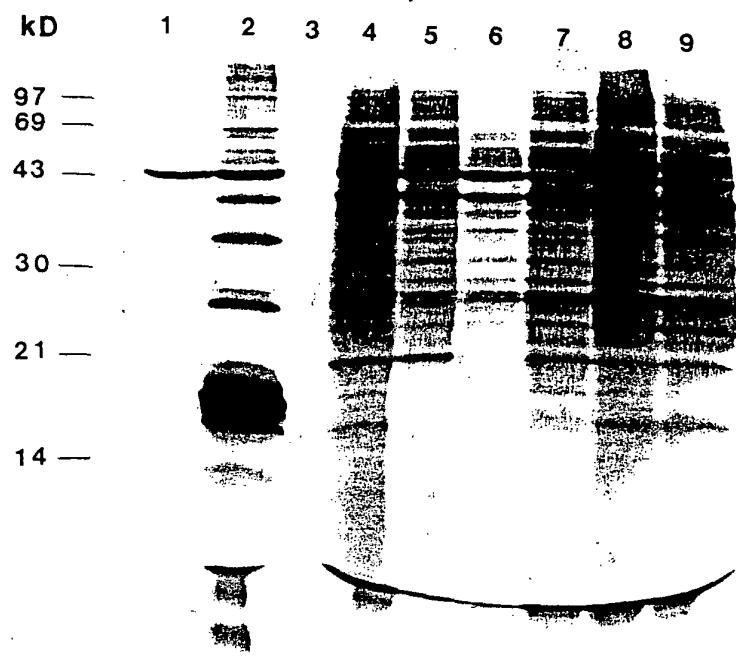


FIG 2.1

09376796 060204

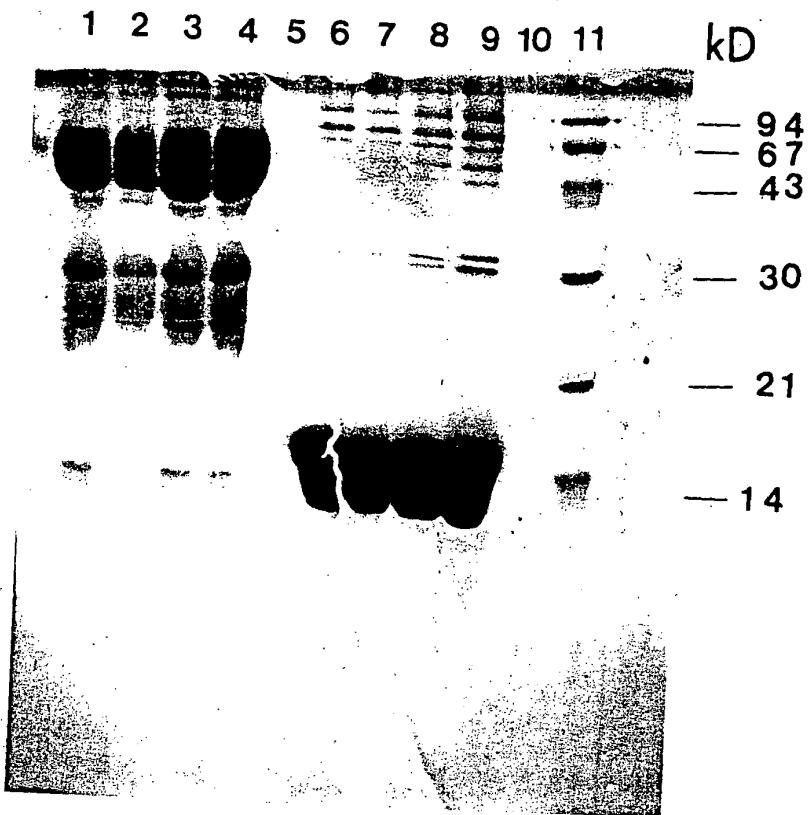


FIG 2.2

00326296 "0602004

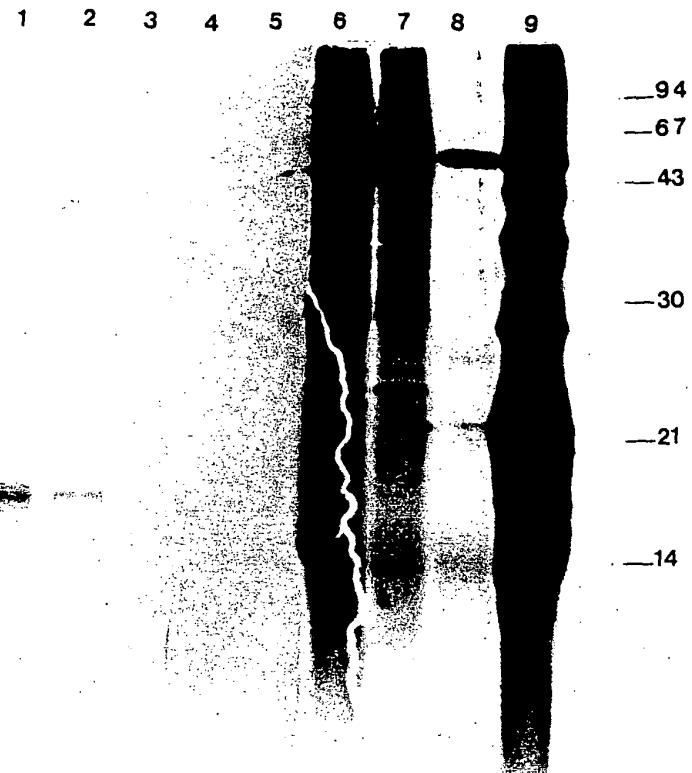


FIG 2.3

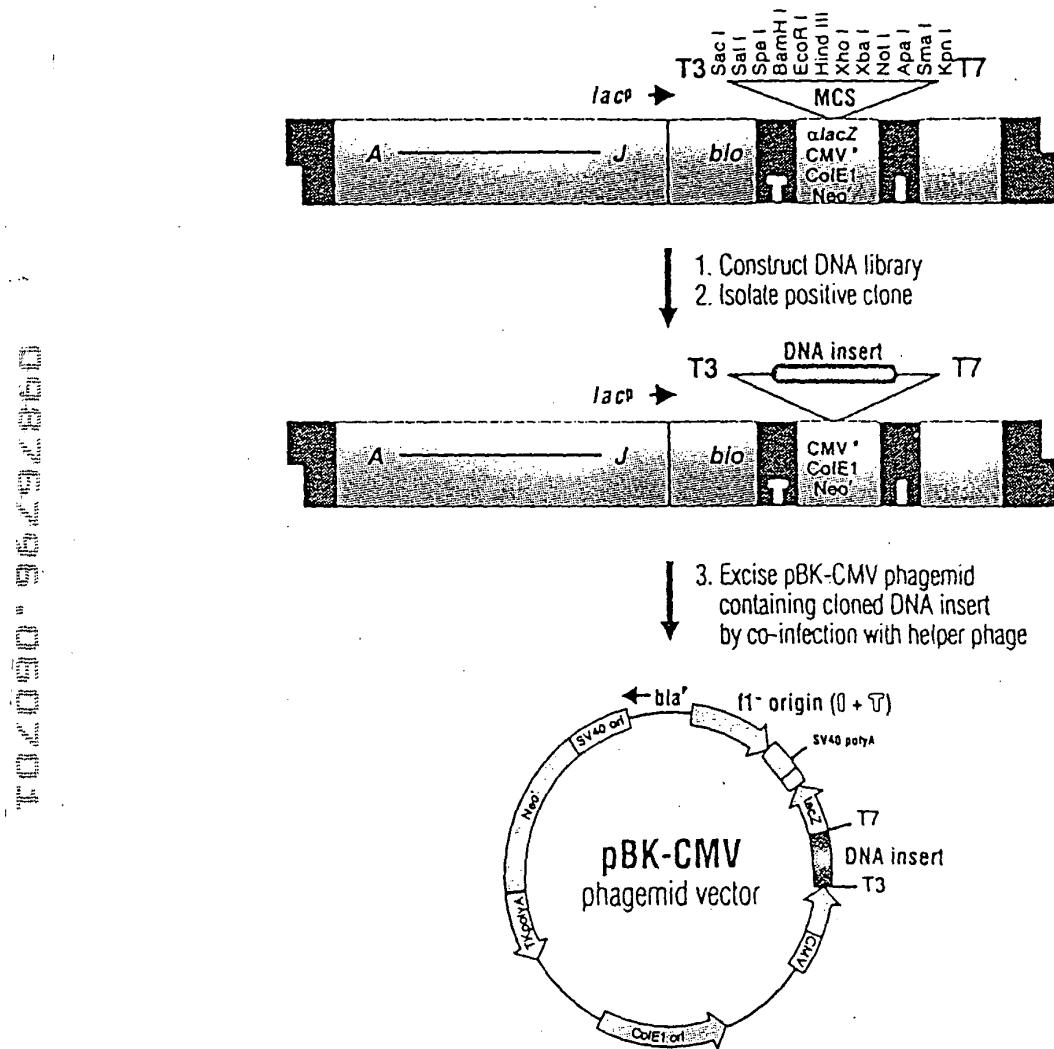
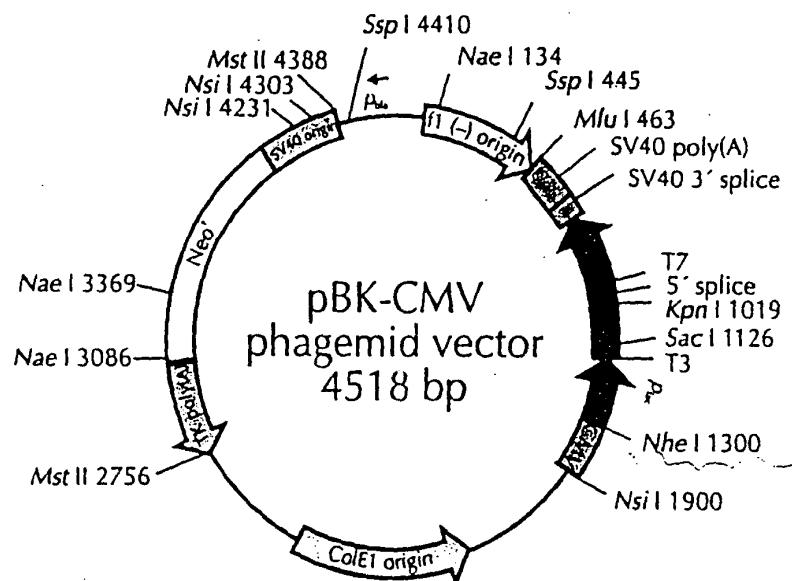


FIG. 2.4 a



BK Reverse Primer
5' ACAGGAAACAGCTATGACCTTG 3'

T3 Primer
5' AATTAACCTCACTAAAGGG 3'

1200 MET T3 promoter +1 →

1183 β-Galactosidase →

Hind III **Xba** I **Xba** I **Not** I **Apa** I **Cla** I **Sma** I **Kpn** I

5' TCACACAGGAAACAGCTATGACCTTGATTAGGCCAACCTCGAAATTAAACCCCTACTAAAGGGAAACAAAAGCTGGAGTCGCGCGCCTGCAGGTCGACACTAGTGGATCCAAG 3'

3' AGTGTGTCTTGTGCGATCTGGAAATAATGGGGTTCACCTTAAATTGGGAGTCATTTCCTGTTTGACCTTGAGGCTTCAAGGGGATATCACTCAGCATAATGTTAAGTGAACGGCAGCCTGATCACCTAGGTTCTAA

Pst I **Bsh** II **Sai** I **Sac** I **Bam** I **ECOR** I

AATTCAAAAAGCTTCTGAGAGACTTCTAGAGGCCGGGGCCATGATTTCAACCCGGGTGGGGTACCAAGGTAAGTACCCATTGGCCCTATAGTGAATGCTTACATTCACACTGGCCGTGTTTACA 3' (+)

GTTTTGAAAGAGCTCTCATGAAGATCTCGCCGGCCGGTAGCTAAAGGTGGGGCCACCCATGGTCAAGGGTTAACGGGGATATCACTCAGCATAATGTTAAGTGAACGGCAGCAAAATG 3' (-)

← +1 T7 promoter

5' CGGGATAATCACTCAGCATAATG 5' TGAACGGCAGCAAAATG 5' T7 Primer M13-20 Primer

FIG. 2.4 b

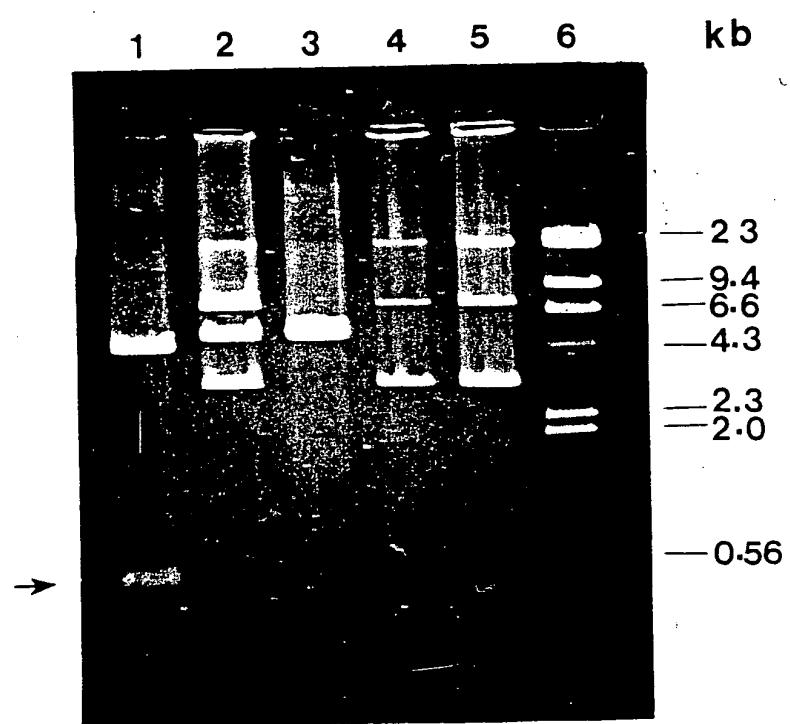


FIG 2.5

DNA sequence of Tm 13.17 cDNA clone

B E
a C
m O
H R
I I

1 AGTGGATCCAAAGAATTGGCACGAGACTACTAACATGAAGTTGCTCTGTTGTCTAACATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAATGTCAAAATGAAAGTGGAGTGTGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAATGGGAGGACGATCCTAAACTGAAACGCCAAGTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCACGGAATCGGGAGAGGTGGTGGTGCACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCCTCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTCAATACTTCAAATGTGTCAATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAAGTGTGATTGAACCACACGACTAGTAGATGGTCAAATGGTGTGCTTTAC
F S P V D *

X
h
o
i

481 ATATAAAAATAAGTGTCTGATGTAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

FIG 2.6a

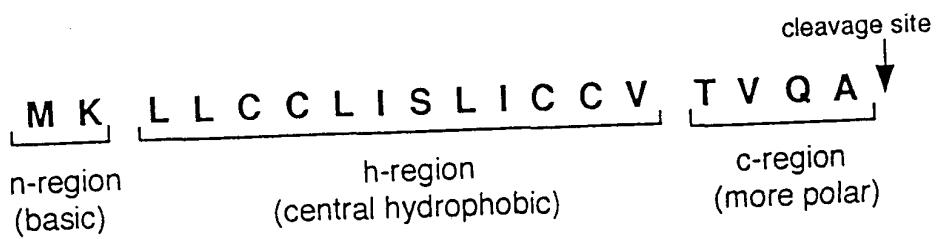


FIG 2.6b

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR
51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN
101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

FIG 2.6c

卷之三

1	AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAAGATGAA	Tm 13.17 B 1
41	OTTOCTCTOTTOCTCTAATCTCTCCCTCATTCGTTGOTCAACAA	Tm 13.17 B 1
1	CTTACTTCTCTCATTCGTTGOTCAACAA	
81	OTTCAGGCCCTGACCGAGGCAACAAATTGAGGAACTGACCA	Tm 13.17 B 1
28	OTTCAGGCCATRACTGAGGAGACCTTGAGCTRACTGCCCCC	
121	AGATTCAGCAAAATGATGATGAAATGAGTGGAGTGTGCGCA	Tm 13.17 B 1
68	AGACCCAGCGCAGAGTGCAGAGCTGAGGAGTGTGCGCA	
161	AGACATCATGAACTGAAAGCTCGGCAACCGTCACTGGGAGGAC	Tm 13.17 B 1
118	AGACGTCATGAAAGAGCTCGGCAACCGTCACTGGGAGGAC	
201	GATTCCTTAACTGAAACCGCAAGCTCGGCAACCGTCACTGGGAGGAG	Tm 13.17 B 1
148	GACCCCCCAAACTGAAACCGCAAGCTCGGCAACCGTCACTGGGAGGAG	
241	ACGCCCGGTCTGGCCCAAGGAAATCGGGAGAGGAGGTTGGTGGTCGAA	Tm 13.17 B 1
188	CACTCGGAAATAGTCGCGGAAATCGGGAGAGGAGGTTGGTGGCCGAA	
281	CGTGTGTTGAGGGAGGAGGTTGAGGAGGTTGAGGAGGTTGAGGAGGAGC	Tm 13.17 B 1
228	CACGTTCAAGGGAGGAGGTTGAGGAGGTTGAGGAGGTTGAGGAGGAGT	
321	GAAGAAACTGAGAAATCATCAATTAAGTGCCTCGCTCAAGA	Tm 13.17 B 1
268	GAAGAAAGCGAGAGGATTTGTCGAGAGAGTGCACCGGGTGAAGTC	
361	GAGGATACGTGAGAGGAGCGGTGTTCAATACCTTCAARTG	Tm 13.17 B 1
308	AAACACACTCCGGAAAGATACGCCATTTCAGTTAACACGAAATG	
401	TGTCATGAAACAGAGGAGCGTTCCTCACCAAGTTGATTGAA	Tm 13.17 B 1
348	TGTTATTGAGGAGCAAGGCCATTTCT	
441	ACCAACACGAGACTAGTAACTGAGTGGTTCTGAGTGTGCTTTAAC	Tm 13.17 B 1
388	ACGAGACTAGTAACTGAGTGGTTCTGAGTGTGCTTTAAC	
481	ATATTAACGAGACTAGTAACTGAGTGGTTCTGAGTGTGCTTTAAC	Tm 13.17 B 1
428	GCACCAA	

FIG 2.7

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSQEIITKARNGDWEDDPKLKRQVFCVARNA 52
	 : .. . : : : ..
AFP-3	1	ETPREKLQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRA 50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTNDNEETEKIINKCAVKRDTVEETVFNTF 102
		: .. . : ::. .. .::: .::: . : .: ..
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFF 100
Tm 13.17	103	KCVMKNKP 110
		. :
AFP-3	101	KCVHDNRS 108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

FIG 2.8

000000000000000000000000

Tm 13.17

AFP-3

B Protein

M	K	L	L	C	C	L	I	S	L	I	L	L	V	T	V	Q	A
M	K	L	L	L	C	L	V	L	V	A	L	V	A	A	T	Y	A
L	T	S	L	I	L	I	L	L	V	A	V	Q	A				

FIG 2.9

093220Z MAR 90

Tm 13.17 NH₂-L T E A Q I E K L N K I S K K C Q N E
Tm 12.86 NH₂-L T D E Q I Q K R N K I S K E ? Q Q V

FIG 2.10

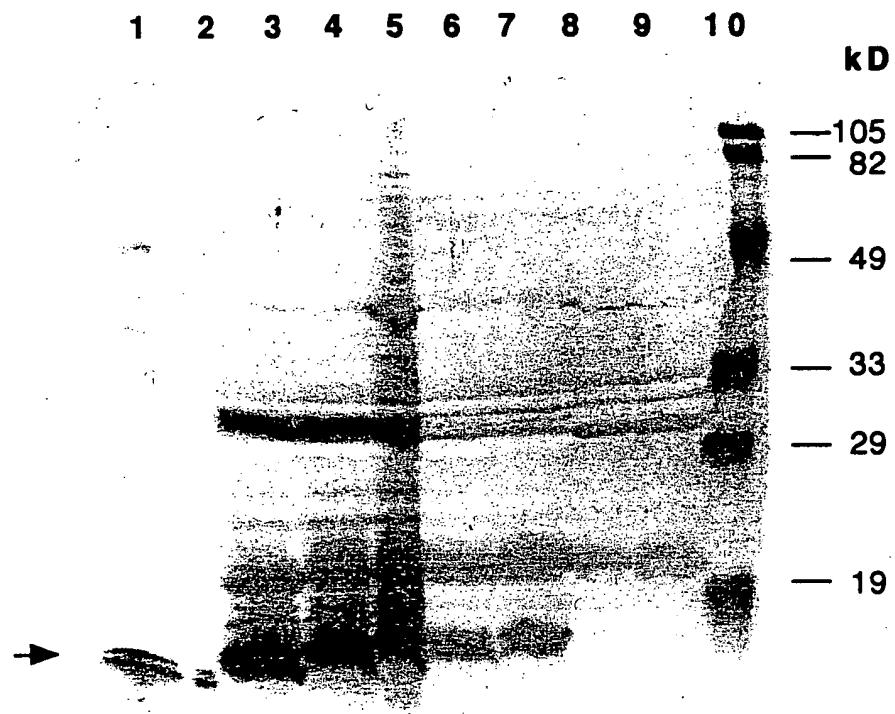


FIG 2.11

0922360

Tm 12.86	1	L T D E Q I Q K R N K I S K E ? Q Q V		
Tm 13.17	1	L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A	30	
B1	13	I T E E D L E L R Q T S A E C K T E S G V S E D V I K R A	43	
AFP-3	1	E T P R E K L K Q B S D A C K A E S G V S E E S L N K V	28	
Tm13.17	31	R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E	60	
B1	44	R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E	74	
AFP-3	29	R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E	58	
Tm13.17	61	V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K	90	
B1	75	I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T	105	
AFP-3	59	F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K	88	
Tm13.17	91	R D T V E E T V F N T F K C V M K N K P K F S P V D	116	
B1	106	E D T P E D T A F E V T K C V L K D K P N F F G D L F V	124	
AFP-3	89	K D T P Q H S S A D F F K C V H D N R S	108	

FIG 2.12

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTGCGTTCGCCGCC
 M K L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA
 I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAACTGGA
 P K M K H V L C F S K K T G

226 GTGGCAACCGAACGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V

316 CAGAACGTGCGTGGTCAAGAACGCCACACCAAGAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTCTCTCCT
 D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTTTGACAATAAAAGGT
 I D

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAA

poly (A) tail

FIG 3.0

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTGTCTTCGCCGCC
 M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA
 I V I G A Q A L T D E Q I Q K

92 AGGAACAAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAATGGA
 P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAAGATCGTG
 K L K H V A S D E E V D K I V

316 CAGAACGTGCGTGGTCAAGAACGCCACACCAAGAGGAACGGCTTAT
 Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
 D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTTGACAATAAAGGT

polyadenylation signal

451 ACTATCGTTATGAAAAA
 poly (A) tail

FIG 3.1

start



2-2	GGC ACGAGCAAAATGAAACTCCTCTTGTGCTTTGC
2-3	GGC ACGAGCAAAATGAAACTCCTCTTGTGCTTTGC
2-2	TT CGCCGCCATCGTCATCGGAGCTCAGGCTCTCACCG
2-3	TT CGCCGCCATCGTCATCGGAGCTCAGGCTCTCACCG
2-2	ACGAACAGATACAGAAAAGGAACAAAGATCAGCAAAGA
2-3	ACGAACAGATACAGAAAAGGAACAAAGATCAGCAAAGA
2-2	ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC
2-3	ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC
2-2	GACAAAGTCCGCACAGGTGTCTTGGTCGATGATCCCCA
2-3	GACAAAGTCCGCACAGGTGTCTTGGTCGACGATCCCCA
2-2	AAATGAAGAACGCACGTCCTCTGCTTCTCGAAAGAAAAC
2-3	AAATGAAGAACGCACGTCCTCTGCTTCTCGAAAGAAAAC
2-2	TGGAGTGGCAACCGAACGCCGGAGACACCAATGTGGAG
2-3	TGGAGTGGCAACCGAACGCCGGAGACACCAATGTGGAG
2-2	GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG
2-3	GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG
2-2	AAGAGGTGGACAAGATCGTGCAGAAGTGC GTGGTCAA
2-3	AAGAGTGGACAAGATCGTGCAGAAGTGC GTGGTCAA
2-2	GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC
2-3	GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC
2-2	AAGTGTATTACGACAGCAACCTGATTCTCTCCTA
2-3	AAGTGTATTACGACAGTAAACCTGATTCTCTCCTA
2-2	TTGATT [*] AATTGTTTGTATTTGACTGAATTGACAA
2-3	TTGATT [*] AATTGTTTGTATTTGACTGAATTGACAA
2-2	TAAAGGTAAATATCGTTATGTAAAAAA
2-3	TAAAGGTAACTATCGTTATGAAAAAA

FIG 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG 3.3

09826296-060204

0 9 8 7 6 5 4 3 2 1 0

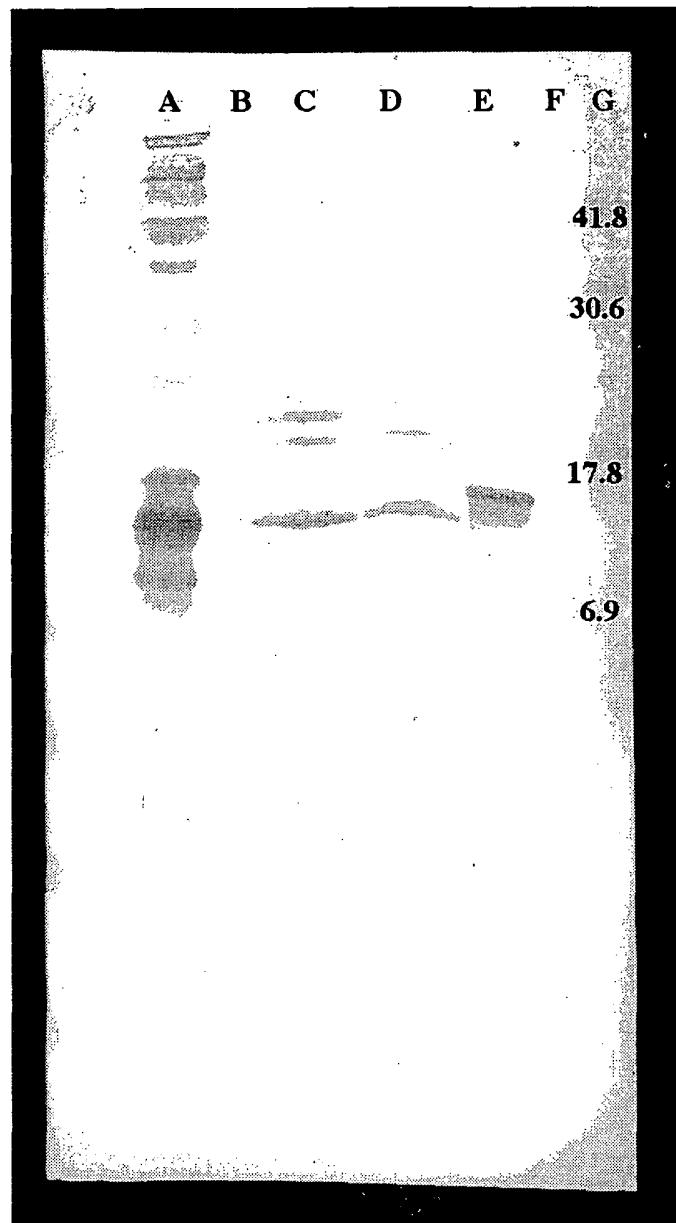


FIG 3.4

Lane

1 2 3 4 5

a→

b→

←**a**

←**b**

577 bp

483 bp

FIG 4.0

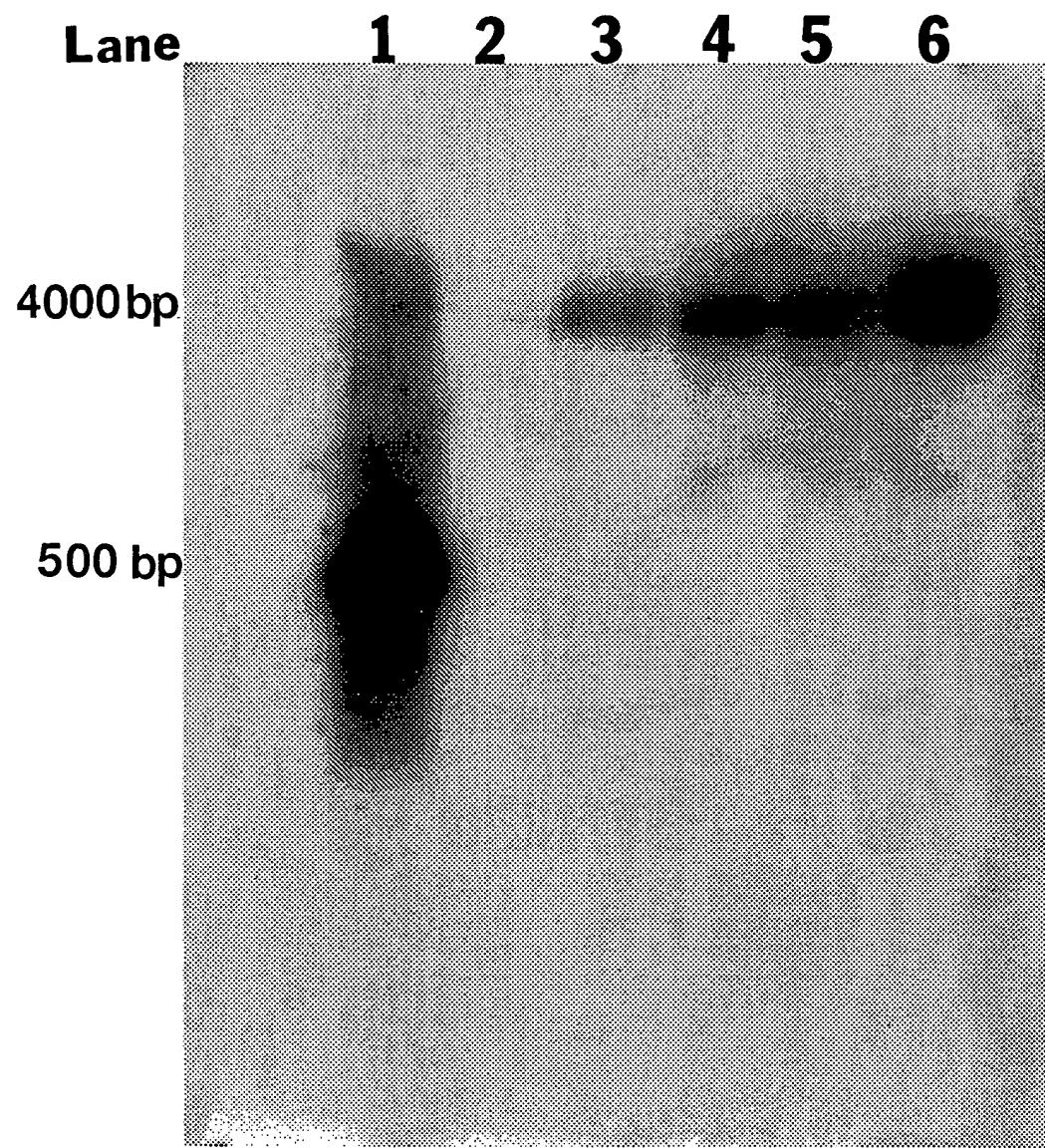


FIG 4.1

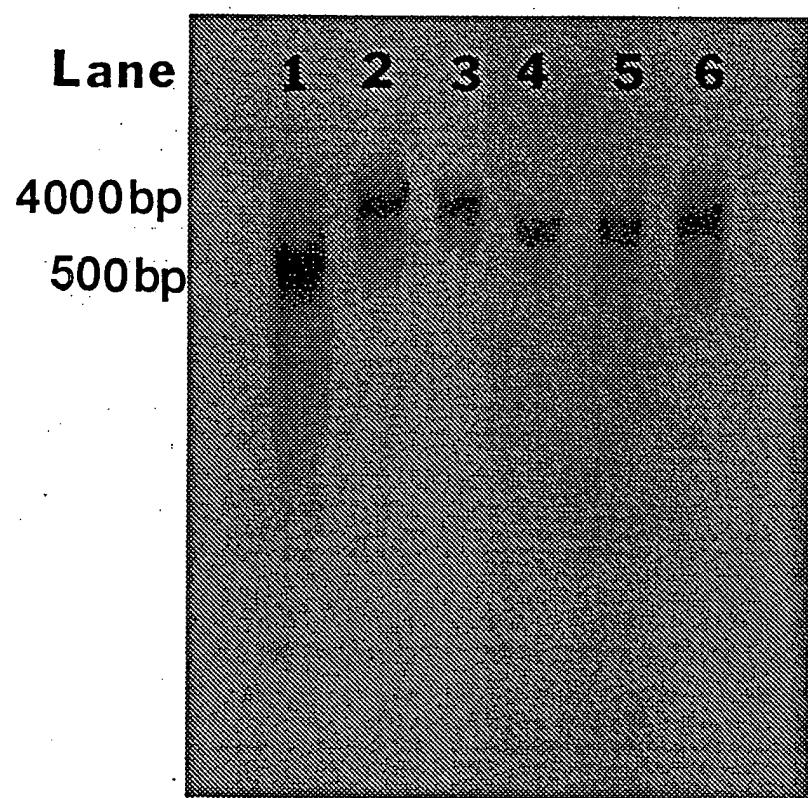


FIG 4.2

FIGURE 4.0 "Gel Electrophoresis"

A.

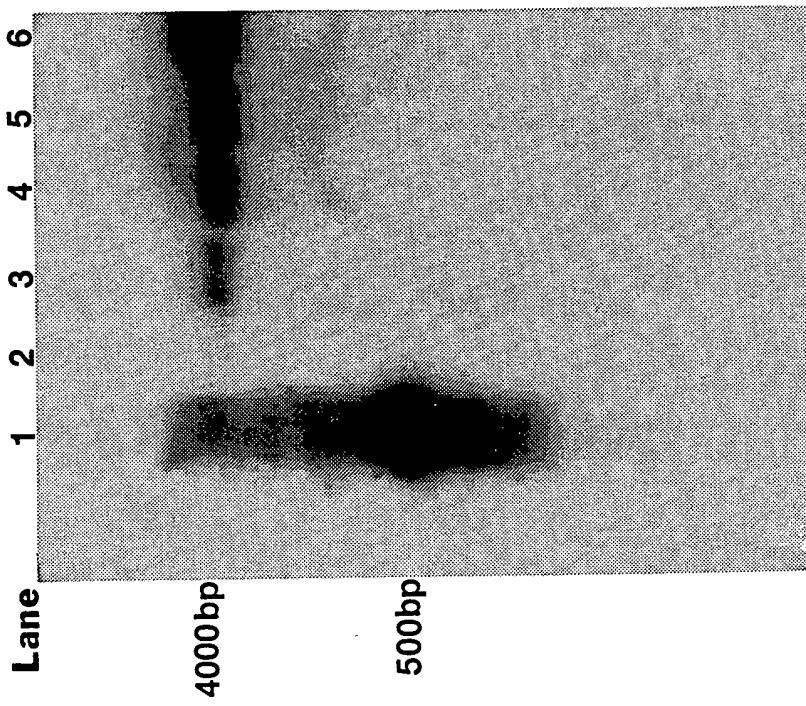
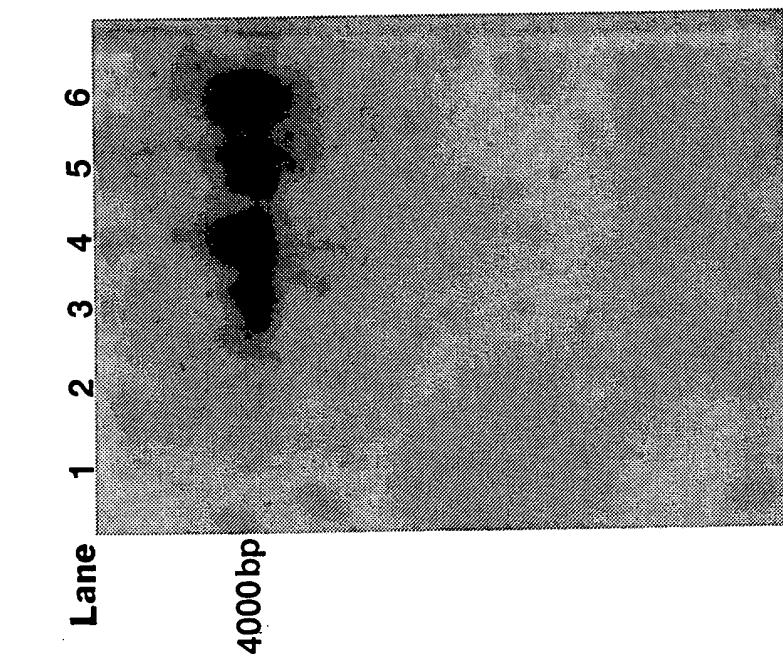


FIG 4.3

7 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

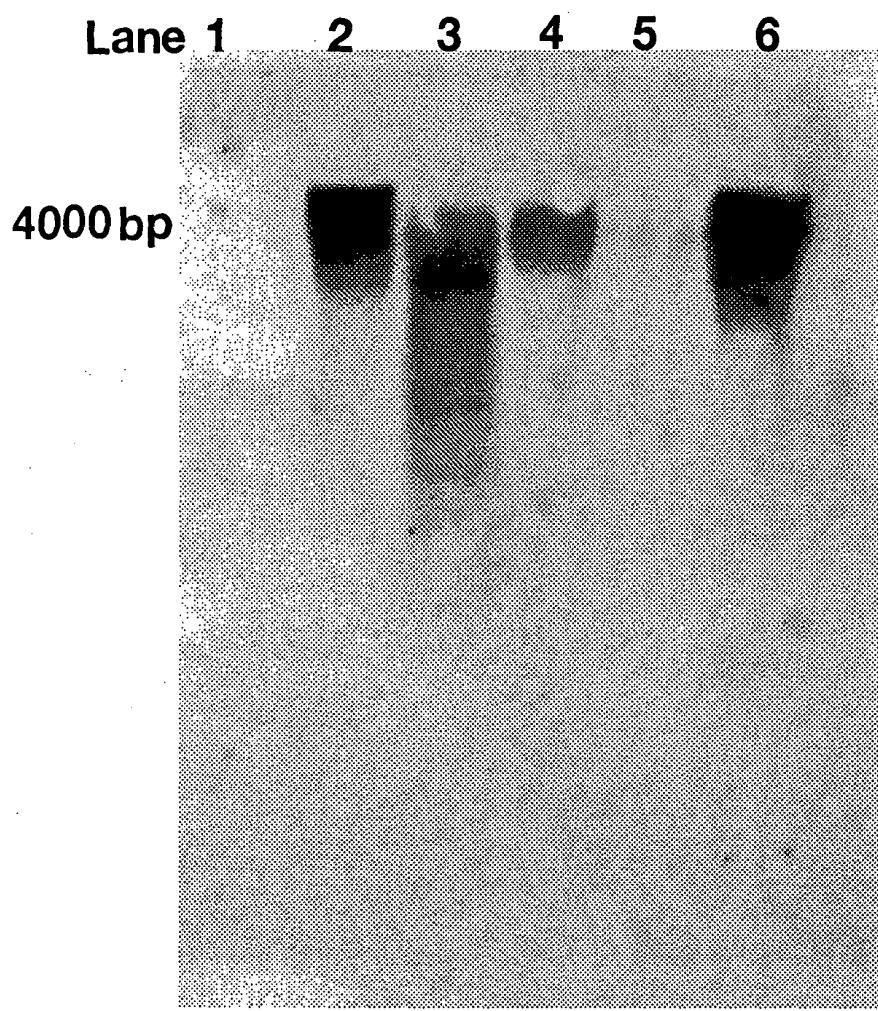


FIG 4.4

Lane **1** **2** **3** **4** **5**



23130

9416

4361

2322

2027

564

FIG 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTGGCACGAGACTACTAAGATCAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAATGTCAAAATGAAAGTGGAGTGTCGCAAGAGATCATAACCAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTGTGGCCAGGA
N G D W E D D P R L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGATCGGGAGAGGTGGTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCAATAACTTTCAAATGTGTCATGAAAAACAAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTACCAGTTGATTGAACCACCGACTAGTAGATGGTCAAATGGTGTGCTTAC
F S P V D *

481 ATATAAAAATAAAGTTTCTGATGTAAAAAAAAAAAAAAAAAAAACTC

FIG. 4.6 a

B.

Forward Primer

2-2	LT D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
Tm 13.17	L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A R N G D W E
B2	L T E E D L Q L L R Q T S A E C K T E S G A S E A V I K K A R K G D L E
AFP-3	E T P R E K L K Q H S D A C K A E S G V S E E S L N K V R N R E E V

2-2	D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H
Tm 13.17	D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K
B2	D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R
AFP-3	D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E

Reverse Primer

2-2	V A S D E E V D K I V Q K C V V K K A T P E E T A Y D T F K C I Y D S
Tm 13.17	V T D N D E E T E K I I N K C A V K R D T V E E T V F N T F K C V M K N
B2	V T N D D E E S E K I V E K C T V T E D T P E D T A F E V T K C V L K D
AFP-3	N S E H P E K V D D L V A K C A V K K D T P Q H S S A D F F K C V H D N

2-2	K P D F S P I D
Tm 13.17	K P K F S P V D
B2	K P N F F G D L F V
AFP-3	R S

09080625 09080625

C.

percent % composition

Primer	A	C	G	T	Melting Temperature (°C)
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

FIG 4.6

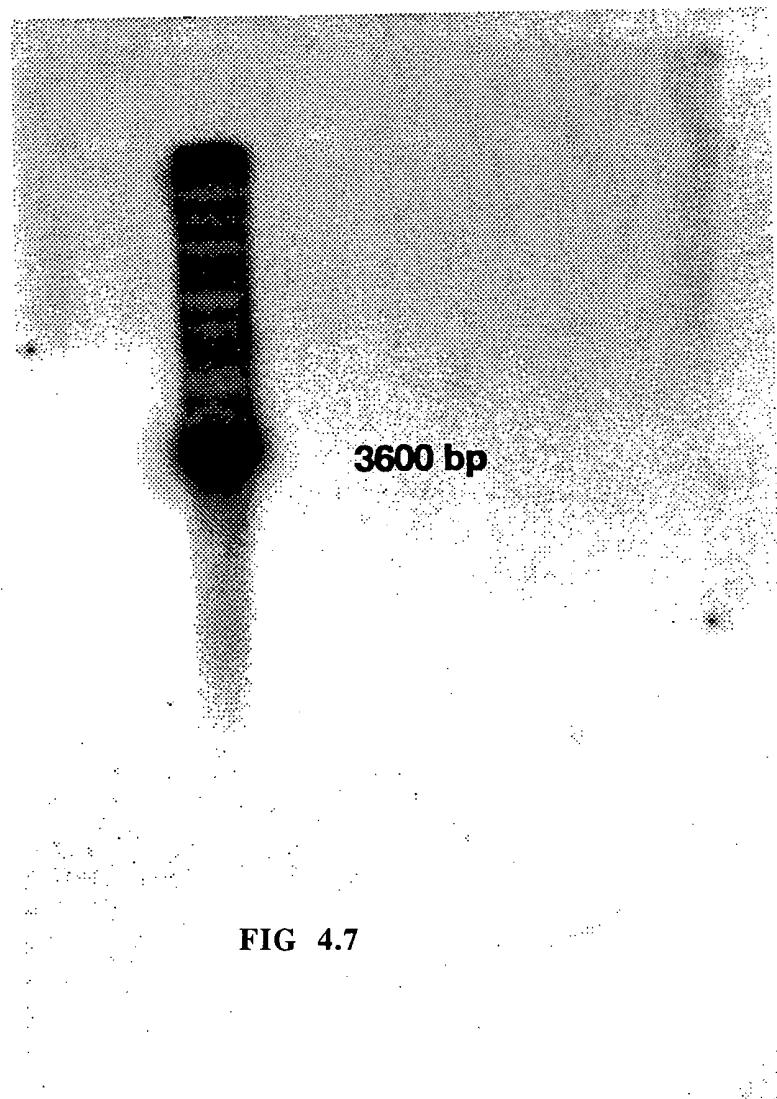


FIG. 4.7

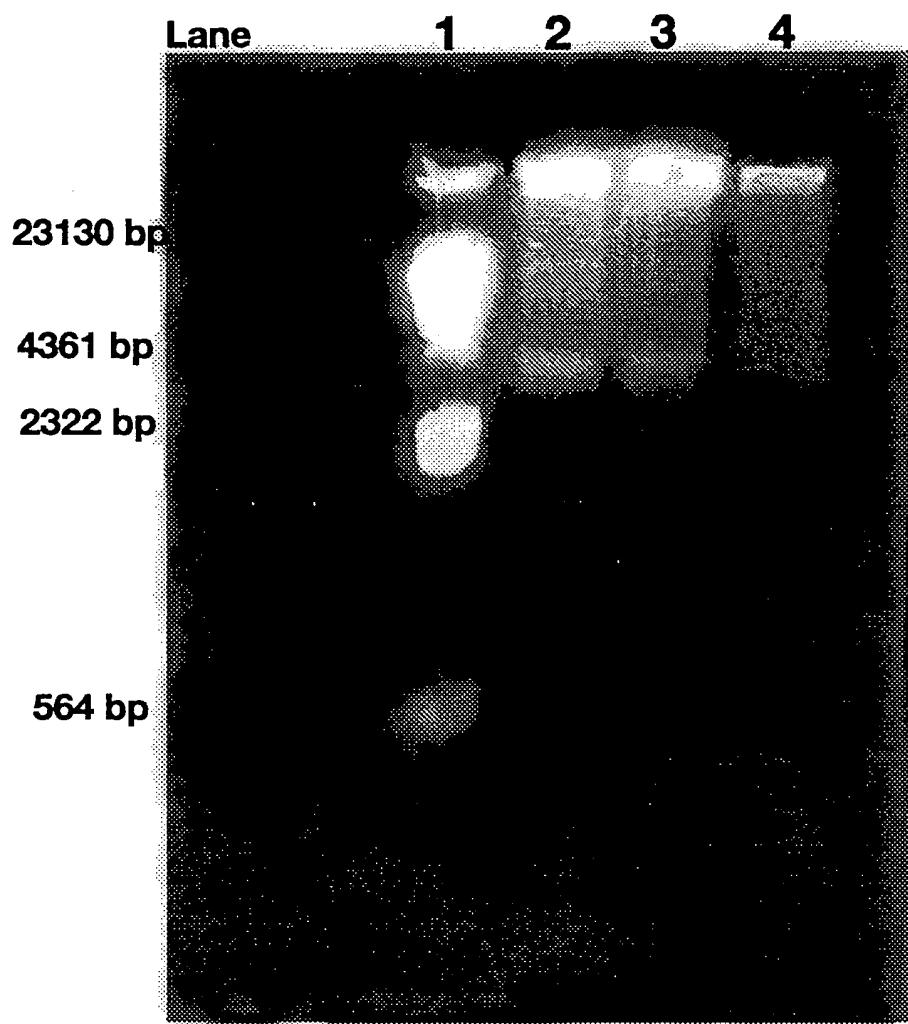


FIG 4.8

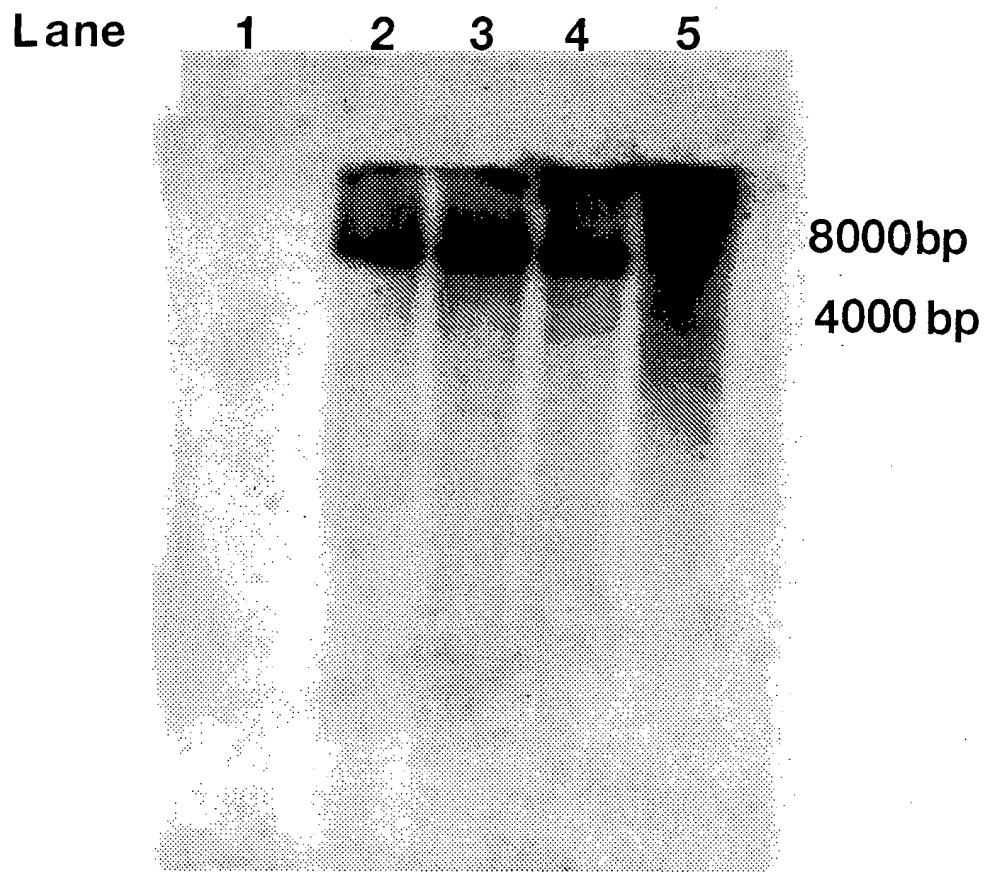


FIG 4.9

poly (A) tail

polyadenylation signal

FIG. 4.10 a

Analysis	Whole Protein
Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Predicted Amino Acid

Composition of 3-4

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AIFFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.10 b

1 GGCACGGAGCAAAA ATGAAACTCCTCTTGTGCTTGTCTTCGCCGCC
 M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATAACAGAAA
 I V I G A Q A L T D E Q I Q K

92 AGGAACAAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
 R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAACGACCGTCCCTCTGCTTCTCGAACAGAGAACTGGA
 P K M K K H V L C F S K R T G

226 GTGGCAACCGAACGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAACGTGGACAAAGATCGTG
 K L K H V A S D E E V D K I V

316 CAGAACGTGCGTGGTCAAGAACGCCACACCAAGAGGAACGGCTTAT
 Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTACGACAGTAAACCTGATTTCTCTCCT
 D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTGACAATAAGGT
 I D

polyadenylation signal

451 ACTATCGTTATGAAAAA
 poly (A) tail

FIG. 4.11 a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Whole Protein Composition Analysis			
Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AIFFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.11 b

1 GGCACGAGCAAAATGAAACTCCTCTGTGCTTGCGTTCGCCGC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCGAAGAAAACTGG
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAACGTGCGTGGTCAAGAAGAACGCCACACCGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTGTATTTACGACAGTAAACCTGATTTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTATTGTTTGTATTTGGCTGATTTTGACAAAAGGT
I D *

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAA

poly (A) tail

FIG. 4.12 a

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.12 b

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FIG. 4.13

FIGURE 4.14
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2-2 M K L L L C F A F A A | V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S Q E T I D K V R T G V L V
 2-3 M K L L L C F A F A A | V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S Q E T I D K V R T G V L V
 3-4 M K L L L C F A F A A | V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S Q E T I D K V R T G V L V
 3-9 M K L L L C F A F A A | V I G A Q A L T D E Q I Q K R N K I S K E C Q Q E S G V S Q E T I D K V R T G V L V
 7-5 M K L L L C F A F A A | V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V



2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 2-3 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 3-4 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 3-9 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 7-5 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K

2-2 A T P E E T A Y D T F K C I Y D S S K P D F S P I D*
 2-3 A T P E E T A Y D T F K C I Y D S S K P D F S P I D*
 3-4 A T P E E T A Y D T F K C I Y D S S K P D F S P I D*
 3-9 A T P E E T A Y D T F K C I Y D S S K P D F S P I D*
 7-5 A T P E E T A Y D T F K C I Y D S S K P D F S P I D*

FIG. 4.14

(kDa)	MW	(% mole)												Thr	% most hydrophilic								
		AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser			
Tm	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3	
12.86	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.4	0	0	7.12	15.6	3.31	6.14	32.14	
Tm	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1	1	0	0	0	0	0	0	
13.17	2.2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2.2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	0	0	0	0	0	
2.3	3.4	12.84	115	3.21	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
3.4	12.84	115	3.21	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	0	0	0	0	0	
3.9	7.5	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
3.9	12.87	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	0	0	0	0	0	
7.5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	

FIG. 4.15

Digitized by Google

Tm	12.86
2-2	
2-3	
3-4	
3-9	
7-5	
Tm	13.17
B1	
B2	
AFP-3	

2-2
2-3
3-4
3-9
7-5
Tm 13.17
B1
B2
AED-3

2-2
2-3
3-4
3-9
7-5
Tm 13.17
B1
B2
AFP-3

FIG. 4.16

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Trm 13.17
2-2
B1 prot
B2 prot
Pbp_Antpo
Pbp_Manse
Opp1_Manse
Opp2_Manse
Pbpos-E_Drome
Pbpos-F_Drome
Pbprp1_Drome
Pbprp2_Drome

Trm 13.17
2-2
 B1 prot
 B2 prot
 Pbp_Antpo
 Pbp_Manse
 Obp1_Manse
 Obp2_Manse
 Pbps_E_Drome
 Pbps_F_Drome
 Pbpri1_Drome
 Pbpsp2_Drome

FIG. 4.17

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Tm 12.86

2-2
2-3
3-4
3-9
7-5
Tm 13.17
B1
B2
AEB-3

FIG. 4.18

NUCLEOTIDE SEQUENCES

		PERCENT SIMILARITY										
		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm 13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}	
PERCENT DIVERGENCE	1	99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1	2-2
	2	0.9		99	99	99	51.5	43.2	42.7	20.2	21.3	2 ²⁻³
3	1.6	60		98	98	50.3	42	42.1	20	20	3 ³⁻⁴	
4	1.6	20	80		98.4	51.3	43.7	43.6	20.4	22	4 ³⁻⁹	
5	1.8	25	75	45		50.4	42.5	42.9	22.2	23.1	5 ⁷⁻⁵	
6	36.9	36.4	37.2	36.4	37.1		57.2	37.4	23.3	21	6 ^{Tm 13.17}	
7	39.9	41.2	41.7	40.7	41.2	30.2		39.3	21.9	22.1	7 ^{B1}	
8	41.8	42.4	43.1	42.3	42.3	45.3	49.4		21.8	23.1	8 ^{AFP-3}	
9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2		45.6	9 ^{YL-1}	
10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5		10 ^{DAFP-1A}	

AMINO ACID SEQUENCES

		PERCENT SIMILARITY										
		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm 13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}	
PERCENT DIVERGENCE	1	100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1	2-2
	2	0	99.1	99.1	100	51.3	37.4	35.2	11.6	12	2 ²⁻³	
3	0.9	0.9	98.3	99.1	50.4	36.5	34.3	11.6	12	3 ³⁻⁴		
4	0.9	0.9	1.7	99.1	51.3	37.4	36.1	10.7	12	4 ³⁻⁹		
5	0	0	0.9	0.09	51.3	37.4	35.2	11.6	12	5 ⁷⁻⁵		
6	46.1	46.1	47	46.1	46.1		47.4	39.8	13.4	13.9	6 ^{Tm 13.17}	
7	59.1	59.1	60	59.1	59.1	51.7		37	11.6	11.1	7 ^{B1}	
8	61.7	61.7	62.6	60.7	61.7	60.2	63		10.2	8.3	8 ^{AFP-3}	
9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5		55.6	9 ^{YL-1}	
10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2		10 ^{DAFP-1A}	

FIG 4.19

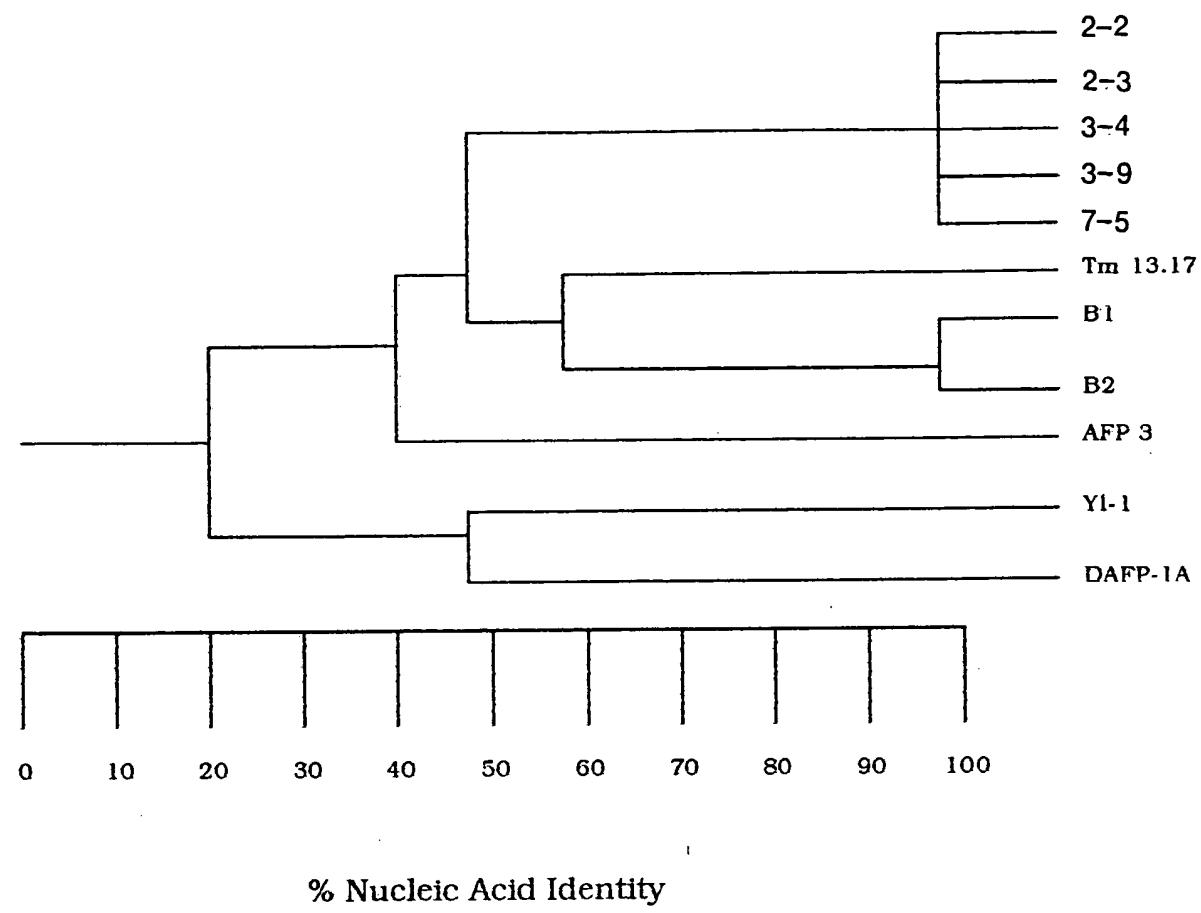


FIG 4.20

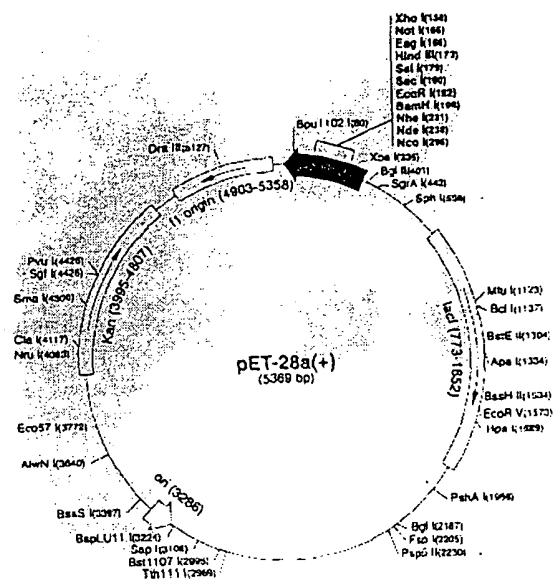


FIG. 5.0

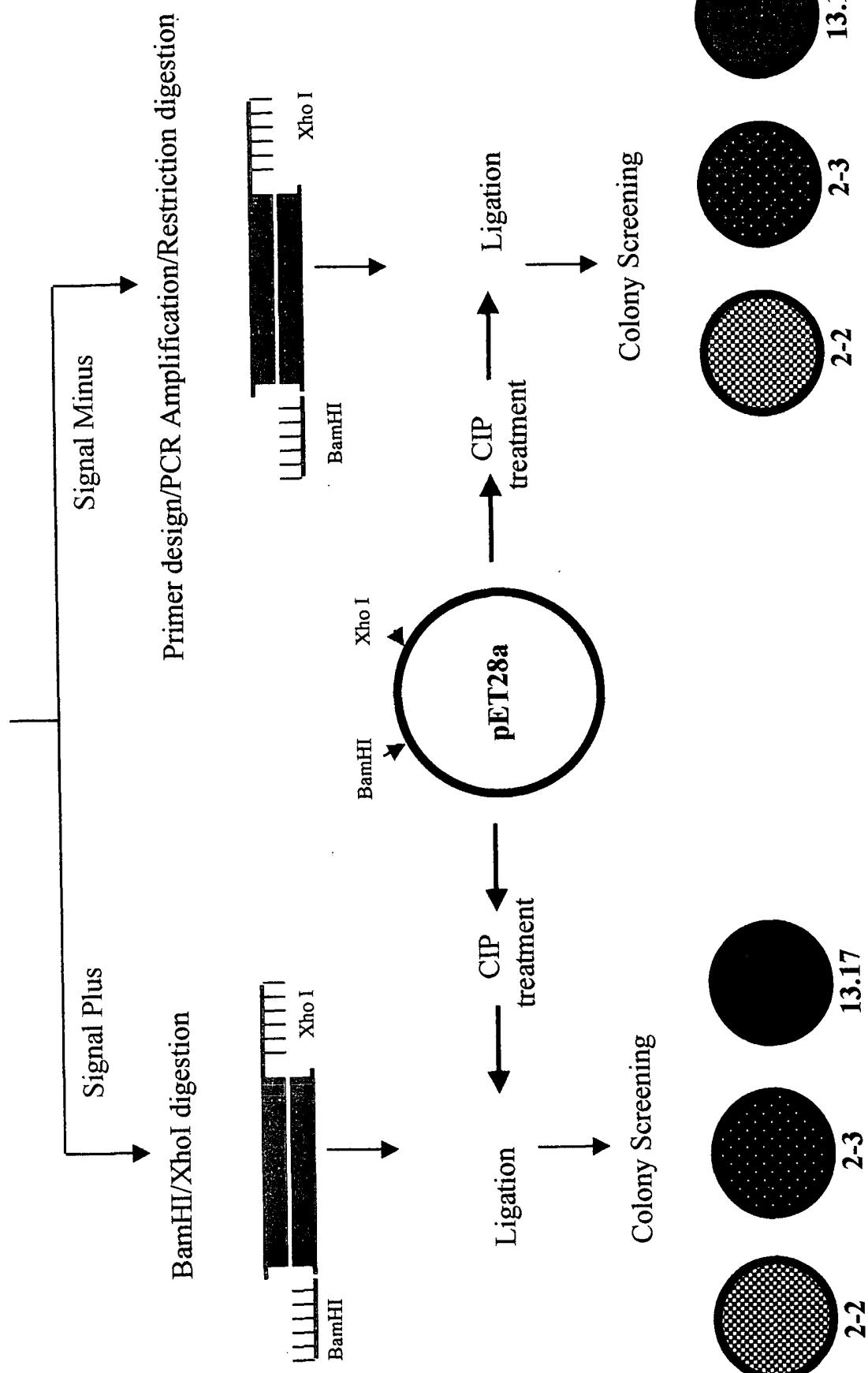
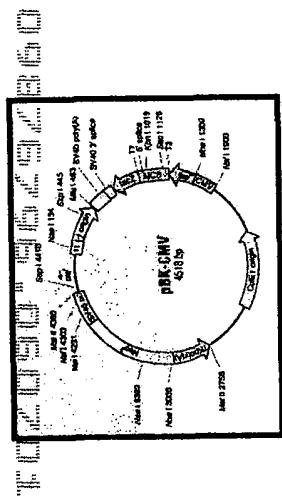


FIG. 5.1

500 bp →

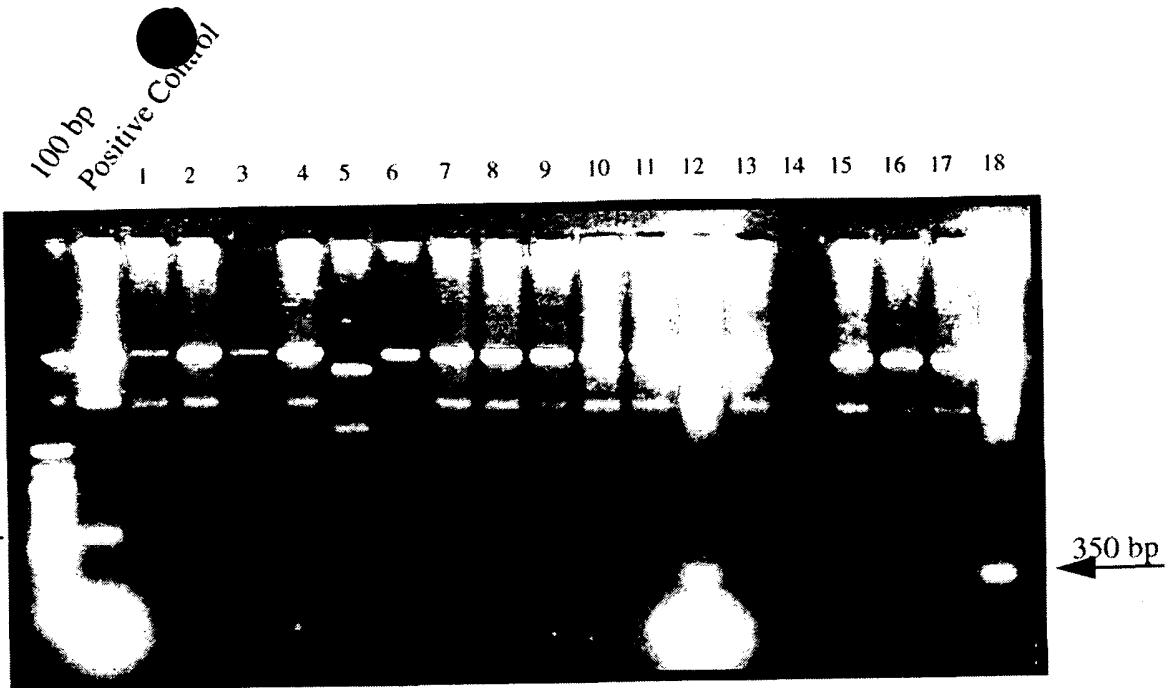


FIG. 5.2

0.9872525E-050001

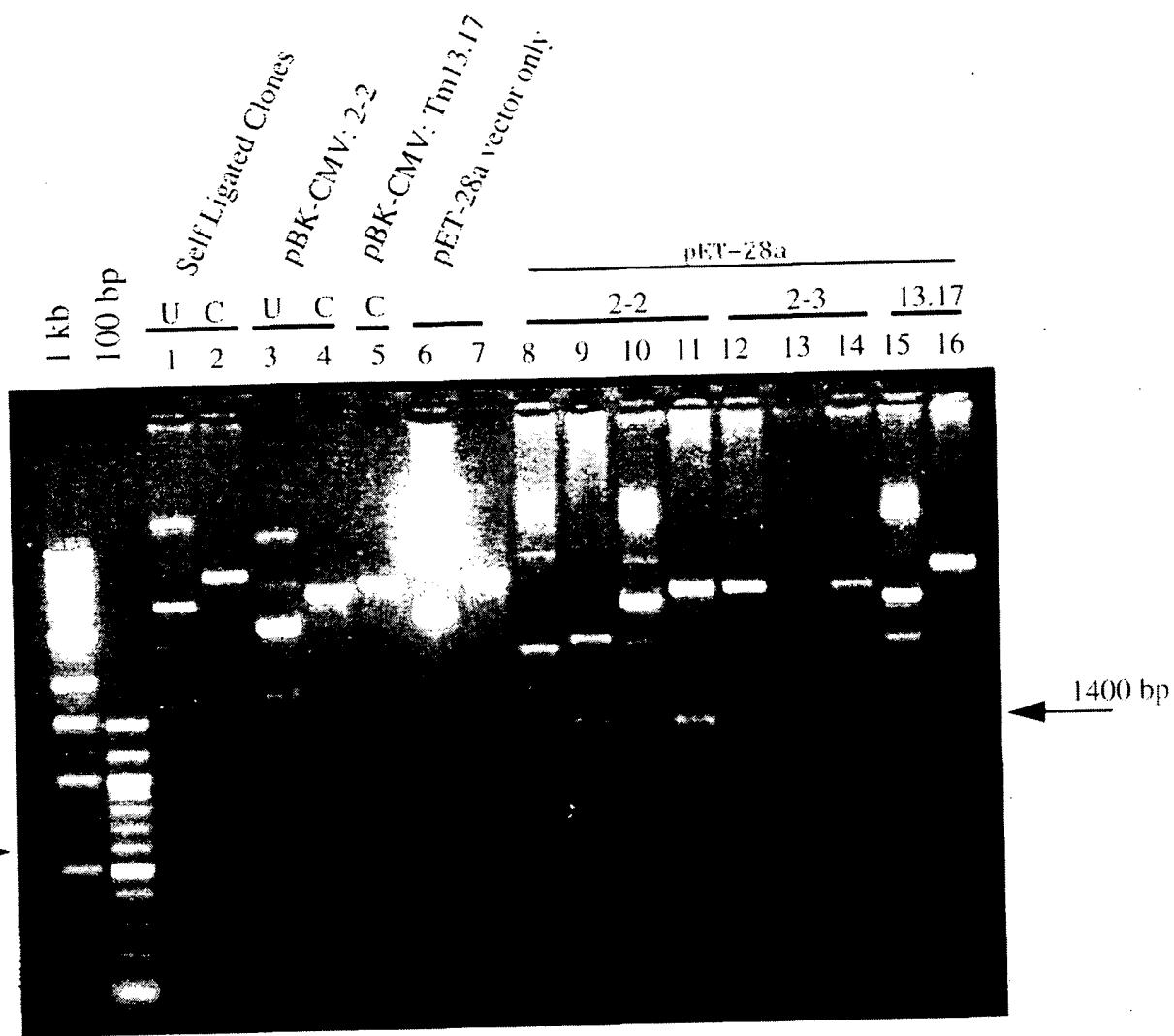


FIG. 5.3

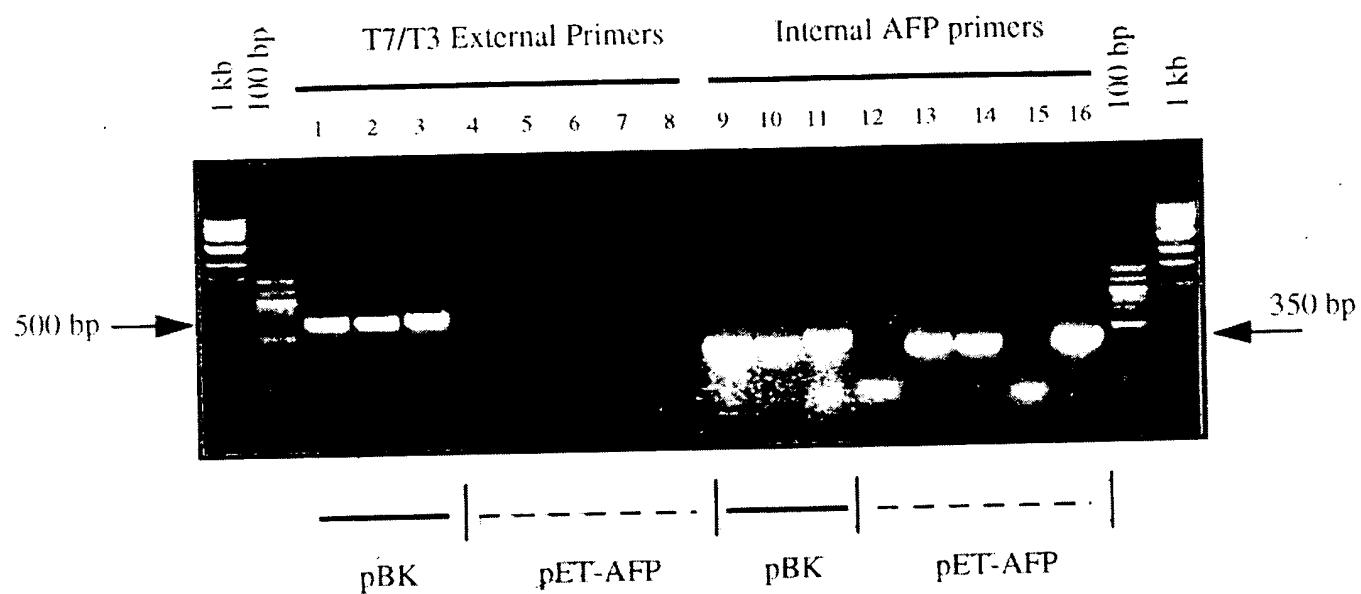


FIG. 5.4

7022620 " 36200

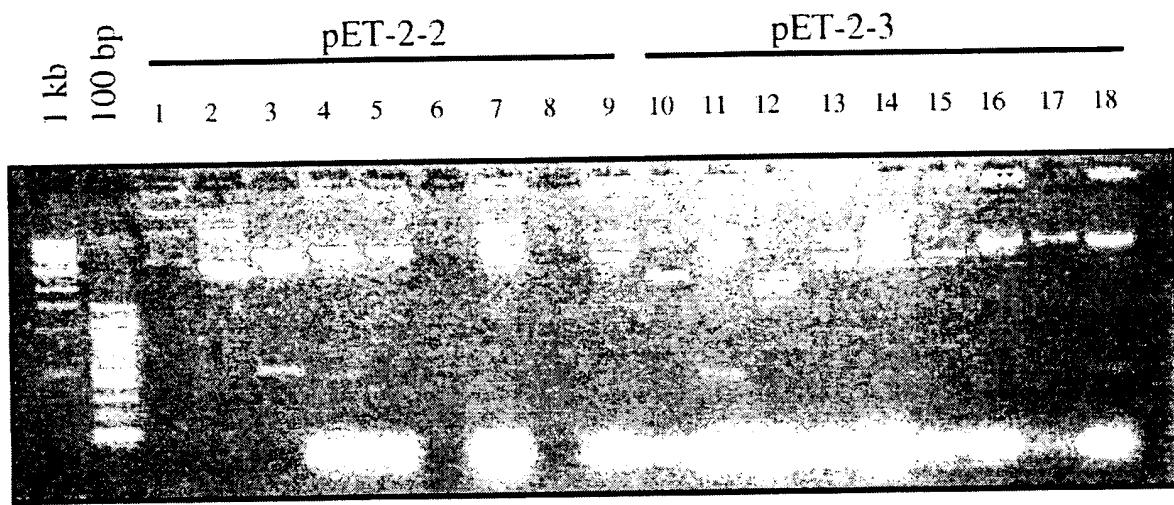


FIG. 5.5

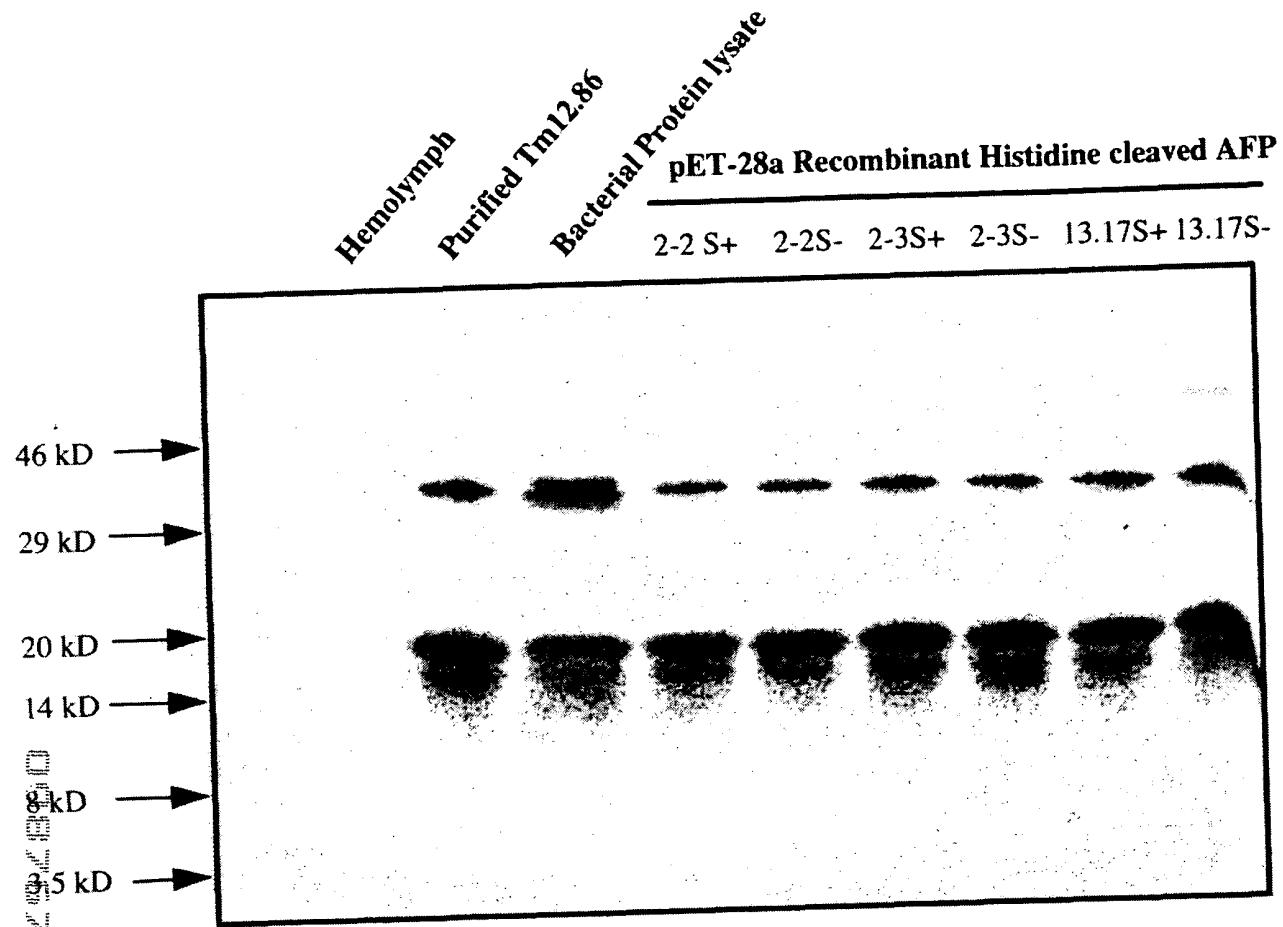


FIG. 5.6

His-tagged Clone 2.2 with signal sequence

FIG. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His His Ser	
-30	-25
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20	-15
-10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5	1
5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10	15
20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25	30
35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40	45
50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55	60
65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70	75
80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85	90
95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100	105
110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACGTGAGAT	543
Pro Ile Asp *	
115	

FIG. 5.8

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50	
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96	
-55	-50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141	
-45	-40	-35
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys <u>Met</u>	186	
-30	-25	-20
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT <u>Lys</u> Leu Leu Leu Cys Phe Ala Ala Ile Val Ile Gly Ala	231	
-15	-10	-5
N-terminal of Mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC <u>Gln Ala</u> Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276	
1	5	10
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321	
15	20	25
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366	
30	35	40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411	
45	50	55
GGA GAC ACC AAT GTG GAG GTC CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456	
60	65	70
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501	
75	80	85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546	
90	95	100
Stop Codon		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595	
105	110	115
Polyadenylation signal Poly-A tail		
TTTGACTGAA TTTTGACAA <u>AT</u> AAAGGTACTA TCGTTATGAA AAAAAAAA	645	
AAAAAAACTC GAGCACCACC ACCACCACTA CTGAGAT	682	

FIG. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30	-25
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20	-15
-10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5	1
5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10	15
20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25	30
35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40	45
50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55	60
65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70	75
80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85	90
95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100	105
110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

FIG. 5.10

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-65 -60 -55	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-50 -45 -40	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile	
-35 -30 -25	
AFP Start Codon	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC	231
Arg His Glu Thr Thr Lys <u>Met Lys</u> Leu Leu Cys Cys Leu Ile Ser	
-20 -15 -10	
N-terminal of mature AFP	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT	276
<u>Leu Ile Leu Leu Val Thr Val Gln Ala</u> Leu Thr Glu Ala Gln Ile	
-5 1 5	
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA	321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly	
10 15 20	
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG	366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu	
25 30 35	
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC	411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn	
40 45 50	
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG	456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu	
55 60 65	
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG	501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu	
70 75 80	
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG	546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu	
85 90 95	
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG	595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys	
100 105 110	
Stop Codon	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG	643
Phe Ser Pro Val Asp *	
115	
Polyadenylation signal Poly-A tail	
TGTGCTTAC ATATAAA <u>AT</u> AAAGTGTTC TGATGTAAAA AAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

FIG. 5.11

His-tagged Tm 13.17 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50	
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser	96	
-30	-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141	
-20	-15	-10
N-terminal of mature AFP		
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	186	
-5	1	5
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	231	
10	15	20
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	276	
25	30	35
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	321	
40	45	50
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	366	
55	60	65
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	411	
70	75	80
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	456	
85	90	95
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	501	
100	105	110
Stop Codon		
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Val Asp *	543	
115		

FIG. 5.12

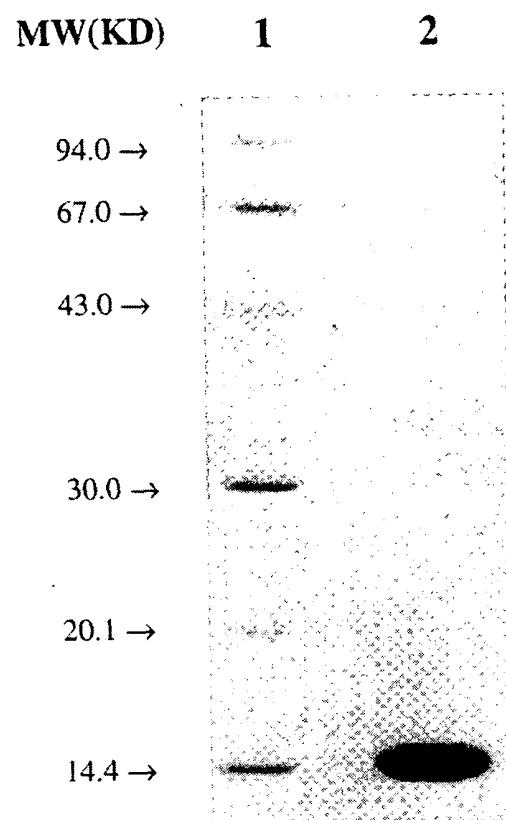


FIG. 6.0

1 2 3 MW(kb)

↔ 34.8

↔ 29.4

↔ 20.9

↔ 7.40

FIG. 6.1

09876796 "060704



FIG. 6.2

Tm 13.17 S- graph data

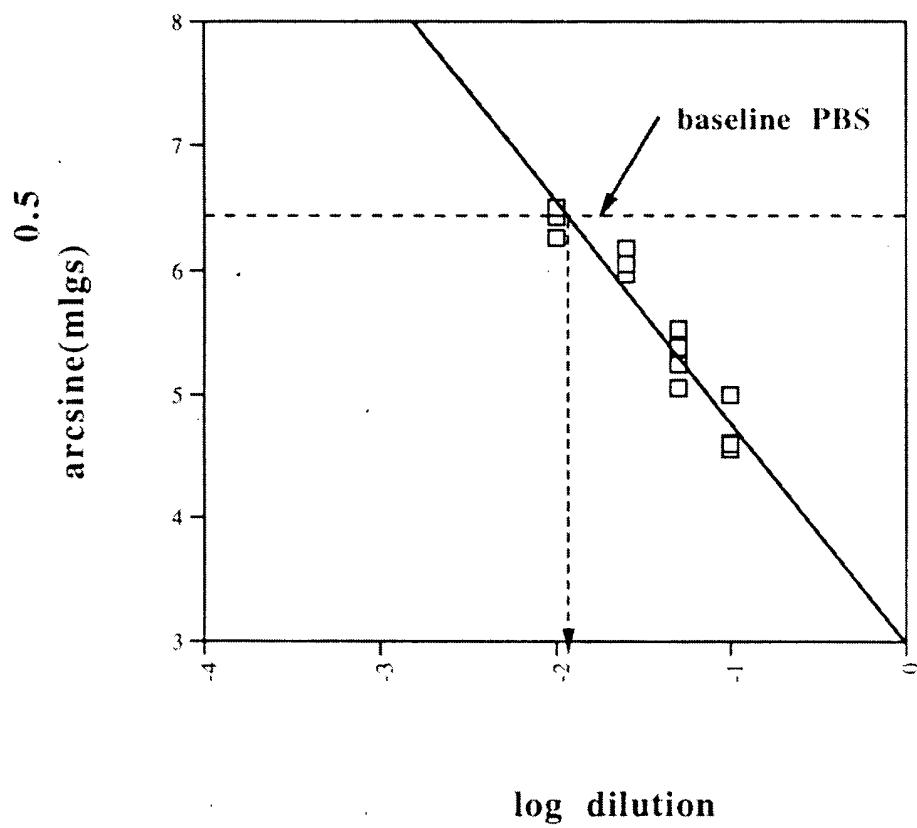


FIG. 6.3

7.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulphydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulphydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

FIG. 7.1

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of Tm 12.84	Tm 13.17	Consensus with Tm 13.17	B1	Consensus with B1	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		C	NN
2	C	C	C	C	C	C	G	N		A	NN
3	G	G	G	G	G	G	A	R		G	NN
4	A	A	A	A	A	A	C	N		A	NN
5	G	G	G	G	G	G	T	N		G	NN
6	C	C	C	C	C	C	A	N		A	NN
7	A	A	A	A	A	A	T	N		A	NN
8	A	A	A	A	A	A	C	N		A	NN
9	A	A	A	A	A	A	T	A		A	NN
10	A	A	A	A	A	A	A	A		A	NN
11	A	A	A	A	A	A	A	A		A	NN
12	A	A	A	A	A	A	A	A		A	NN
13	A	A	A	A	A	A	A	A		A	NN
14	T	T	A	A	A	A	A	A		A	NN
15	G	G	A	A	A	A	A	A		A	NN
16	A	A	A	A	A	A	A	A		A	NN
17	T	T	G	G	G	G	G	G		T	CG
18	G	G	A	A	A	A	A	A		C	CG
19	A	A	A	A	A	A	A	A		C	CG
20	C	C	C	C	C	C	C	C		T	CG
21	T	T	T	T	T	T	T	T		A	CG
22	T	T	T	T	T	T	T	T		T	CG
23	T	T	T	T	T	T	T	T		A	CG
24	C	C	C	C	C	C	C	C		T	CG
25	C	C	C	C	C	C	C	C		A	CG
26	T	T	T	T	T	T	T	T		T	CG
27	T	T	T	T	T	T	T	T		A	CG
28	G	G	G	G	G	G	G	G		T	CG
29	A	A	A	A	A	A	A	A		A	CG
30	G	G	G	G	G	G	G	G		T	CG
31	T	T	T	T	T	T	T	T		A	CG
32	T	T	T	T	T	T	T	T		T	CG
33	G	G	G	G	G	G	G	G		A	CG
34	A	A	A	A	A	A	A	A		C	CG
35	C	C	C	C	C	C	C	C		G	CG
36	T	T	T	T	T	T	T	T		C	CG
37	T	T	T	T	T	T	T	T		G	CG
38	T	T	T	T	T	T	T	T		C	CG
39	G	G	G	G	G	G	G	G		T	CG
40	A	A	A	A	A	A	A	A		A	CG
41	C	C	C	C	C	C	C	C		T	CG
42	G	G	G	G	G	G	G	G		A	CG
43	A	A	A	A	A	A	A	A		C	CG
44	T	T	T	T	T	T	T	T		G	CG
45	C	C	C	C	C	C	C	C		C	CG
46	G	G	G	G	G	G	G	G		G	CG
47	A	A	A	A	A	A	A	A		C	CG
48	T	T	T	T	T	T	T	T		G	CG
49	G	G	G	G	G	G	G	G		C	CG
50	A	A	A	A	A	A	A	A		T	CG
51	C	C	C	C	C	C	C	C		C	CG
52	T	T	T	T	T	T	T	T		G	CG
53	T	T	T	T	T	T	T	T		C	CG
54	T	T	T	T	T	T	T	T		G	CG
55	T	T	T	T	T	T	T	T		C	CG
56	T	T	T	T	T	T	T	T		G	CG
57	T	T	T	T	T	T	T	T		C	CG
58	T	T	T	T	T	T	T	T		G	CG
59	T	T	T	T	T	T	T	T		C	CG
60	G	G	G	G	G	G	G	G		G	CG
61	A	A	A	A	A	A	A	A		C	CG
62	T	T	T	T	T	T	T	T		G	CG
63	C	C	C	C	C	C	C	C		C	CG
64	G	G	G	G	G	G	G	G		G	CG
65	A	A	A	A	A	A	A	A		A	CG
66	T	T	T	T	T	T	T	T		T	CG
67	C	C	C	C	C	C	C	C		A	CG
68	G	G	G	G	G	G	G	G		G	CG
69	A	A	A	A	A	A	A	A		A	CG
70	T	T	T	T	T	T	T	T		T	CG
71	C	C	C	C	C	C	C	C		C	CG
72	G	G	G	G	G	G	G	G		G	CG
73	A	A	A	A	A	A	A	A		A	CG
74	T	T	T	T	T	T	T	T		T	CG
75	C	C	C	C	C	C	C	C		C	CG
76	G	G	G	G	G	G	G	G		G	CG
77	A	A	A	A	A	A	A	A		A	CG
78	C	C	C	C	C	C	C	C		C	CG
79	G	G	G	G	G	G	G	G		G	CG
80	A	A	A	A	A	A	A	A		A	CG
81	T	T	T	T	T	T	T	T		T	CG
82	C	C	C	C	C	C	C	C		C	CG
83	G	G	G	G	G	G	G	G		G	CG
84	A	A	A	A	A	A	A	A		A	CG
85	T	T	T	T	T	T	T	T		T	CG
86	C	C	C	C	C	C	C	C		C	CG
87	G	G	G	G	G	G	G	G		G	CG
88	A	A	A	A	A	A	A	A		A	CG
89	T	T	T	T	T	T	T	T		T	CG
90	C	C	C	C	C	C	C	C		C	CG
91	G	G	G	G	G	G	G	G		G	CG
92	A	A	A	A	A	A	A	A		A	CG
93	G	G	G	G	G	G	G	G		G	CG
94	A	A	A	A	A	A	A	A		A	CG
95	C	C	C	C	C	C	C	C		C	CG
96	A	A	A	A	A	A	A	A		A	CG
97	G	G	G	G	G	G	G	G		G	CG
98	C	C	C	C	C	C	C	C		C	CG
99	T	T	T	T	T	T	T	T		T	CG
100	A	A	A	A	A	A	A	A		A	CG
101	T	T	T	T	T	T	T	T		T	CG
102	C	C	C	C	C	C	C	C		C	CG
103	G	G	G	G	G	G	G	G		G	CG
104	A	A	A	A	A	A	A	A		A	CG
105	T	T	T	T	T	T	T	T		T	CG
106	C	C	C	C	C	C	C	C		C	CG
107	G	G	G	G	G	G	G	G		G	CG
108	A	A	A	A	A	A	A	A		A	CG
109	T	T	T	T	T	T	T	T		T	CG
110	C	C	C	C	C	C	C	C		C	CG
111	G	G	G	G	G	G	G	G		G	CG
112	A	A	A	A	A	A	A	A		A	CG
113	T	T	T	T	T	T	T	T		T	CG
114	C	C	C	C	C	C	C	C		C	CG
115	G	G	G	G	G	G	G	G		G	CG
116	A	A	A	A	A	A	A	A		A	CG
117	G	G	G	G	G	G	G	G		G	CG

FIG. 7.2

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm 13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
119	C	C	C	C	C	C	A	N	A	N	G	N
120	A	A	A	G	G	G	T	N	C	T	C	N
121	G	G	G	G	G	G	G	G	T	G	G	G
122	T	T	T	T	T	T	T	A	A	A	A	A
123	G	G	G	G	G	G	G	A	A	A	A	A
124	T	T	T	T	T	T	G	T	R	T	T	T
125	C	C	C	C	C	C	G	G	A	G	G	G
126	G	G	G	G	G	G	G	G	G	G	G	G
127	G	G	G	G	G	G	G	G	G	G	G	G
128	A	A	A	G	G	G	G	G	G	G	G	G
129	G	G	G	G	G	G	G	G	G	G	G	G
130	T	T	T	T	T	T	T	T	T	T	T	T
131	T	T	T	T	T	T	T	T	T	T	T	T
132	G	G	G	G	G	G	G	G	G	G	G	G
133	T	T	T	T	T	T	T	T	T	T	T	T
134	C	C	C	C	C	C	C	C	C	C	C	C
135	C	C	C	C	C	C	C	C	C	C	C	C
136	A	A	A	A	A	A	A	A	A	A	A	A
137	A	A	A	G	G	G	G	G	G	G	G	G
138	G	G	G	G	G	G	G	G	G	G	G	G
139	A	A	A	G	G	G	G	G	G	G	G	G
140	A	A	A	G	G	G	G	G	G	G	G	G
141	G	G	G	G	G	G	G	G	G	G	G	G
142	A	A	A	G	G	G	G	G	G	G	G	G
143	C	C	C	G	G	G	G	G	G	G	G	G
144	G	G	G	G	G	G	G	G	G	G	G	G
145	A	A	A	T	T	T	T	T	T	T	T	T
146	T	T	T	C	C	C	C	C	C	C	C	C
147	C	C	G	G	G	G	G	G	G	G	G	G
148	G	G	G	G	G	G	G	G	G	G	G	G
149	A	A	A	C	C	C	C	C	C	C	C	C
150	C	C	C	C	C	C	C	C	C	C	C	C
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	G	G	G	G	G	G	G	G	G	G	G	G
155	T	T	T	C	C	C	C	C	C	C	C	C
156	C	C	C	G	G	G	G	G	G	G	G	G
157	G	G	G	G	G	G	G	G	G	G	G	G
158	C	C	C	C	C	C	C	C	C	C	C	C
159	A	A	A	C	C	C	C	C	C	C	C	C
160	C	C	C	A	A	A	A	A	A	A	A	A
161	A	A	A	C	C	C	C	C	C	C	C	C
162	A	A	A	G	G	G	G	G	G	G	G	G
163	G	G	G	G	G	G	G	G	G	G	G	G
164	G	G	G	G	G	G	G	G	G	G	G	G
165	T	T	T	G	G	G	G	G	G	G	G	G
166	G	T	T	T	T	T	T	T	T	T	T	T
167	T	C	T	T	T	T	T	T	T	T	T	T
168	C	T	T	T	T	T	T	T	T	T	T	T
169	T	T	T	T	T	T	T	T	T	T	T	T
170	T	T	T	G	G	G	G	G	G	G	G	G
171	G	G	G	G	G	G	G	G	G	G	G	G
172	T	T	T	C	C	C	C	C	C	C	C	C
173	G	G	G	C	C	C	C	C	C	C	C	C
174	A	T	T	G	G	G	G	G	G	G	G	G
175	G	A	A	C	C	C	C	C	C	C	C	C
176	A	T	T	G	G	G	G	G	G	G	G	G
177	G	T	T	G	G	G	G	G	G	G	G	G
178	A	T	T	G	G	G	G	G	G	G	G	G
179	G	A	A	T	T	T	T	T	T	T	T	T
180	T	C	C	C	C	C	C	C	C	C	C	C
181	C	C	C	C	C	C	C	C	C	C	C	C
182	A	A	A	A	A	A	A	A	A	A	A	A
183	A	A	A	A	A	A	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	T	T	T	T	T	T	T	T	T	T	T	T
189	G	G	G	G	G	G	G	G	G	G	G	G
190	A	A	A	G	G	G	G	G	G	G	G	G
191	A	A	A	G	G	G	G	G	G	G	G	G
192	G	G	G	G	G	G	G	G	G	G	G	G
193	A	A	A	G	G	G	G	G	G	G	G	G
194	A	A	A	G	G	G	G	G	G	G	G	G
195	G	G	G	G	G	G	G	G	G	G	G	G
196	C	C	C	C	C	C	C	C	C	C	C	C
197	A	A	A	C	C	C	C	C	C	C	C	C
198	C	C	C	C	C	C	C	C	C	C	C	C
199	G	G	G	G	G	G	G	G	G	G	G	G
200	T	T	T	C	C	C	C	C	C	C	C	C
201	C	C	C	T	T	T	T	T	T	T	T	T
202	C	C	C	T	T	T	T	T	T	T	T	T
203	T	T	T	T	T	T	T	T	T	T	T	T
204	C	C	C	T	T	T	T	T	T	T	T	T
205	T	G	G	C	C	C	C	C	C	C	C	C
206	G	T	T	T	T	T	T	T	T	T	T	T
207	T	T	T	T	T	T	T	T	T	T	T	T
208	T	T	T	T	T	T	T	T	T	T	T	T
209	C	C	C	C	C	C	C	C	C	C	C	C
210	T	T	T	T	T	T	T	T	T	T	T	T
211	C	C	C	C	C	C	C	C	C	C	C	C
212	T	T	T	T	T	T	T	T	T	T	T	T
213	G	G	G	G	G	G	G	G	G	G	G	G
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	G	G	G	G	G	G	G	G	G	G	G	G
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	C	C	C	C	C	C	C	C	C	C	C	C
222	T	T	T	T	T	T	T	T	T	T	T	T
223	G	G	G	G	G	G	G	G	G	G	G	G
224	A	A	A	G	G	G	G	G	G	G	G	G
225	G	G	G	G	G	G	G	G	G	G	G	G
226	T	T	T	T	T	T	T	T	T	T	T	T
227	G	G	G	G	G	G	G	G	G	G	G	G
228	G	G	G	G	G	G	G	G	G	G	G	G
229	C	C	C	C	C	C	C	C	C	C	C	C
230	C	C	C	C	C	C	C	C	C	C	C	C
231	A	A	A	A	A	A	A	A	A	A	A	A
232	C	C	C	C	C	C	C	C	C	C	C	C
233	C	C	C	C	C	C	C	C	C	C	C	C
234	G	G	G	G	G	G	G	G	G	G	G	G
235	G	G	G	G	G	G	G	G	G	G	G	G

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	G	G	G	G	G	T	N	A	A	CG	N
238	G	C	C	C	C	C	C	C	T	G	GT	CG
239	C	C	C	C	C	C	G	G	C	G	GT	CG
240	C	G	G	G	G	G	G	G	G	G	GT	CG
241	G	G	G	G	G	G	G	G	G	G	GT	CG
242	A	G	G	G	G	G	G	G	G	G	GT	CG
243	G	A	A	A	A	A	A	A	A	A	GT	CG
244	A	C	C	C	C	C	A	A	A	A	GT	CG
245	C	A	A	A	A	A	C	C	A	A	GT	CG
246	A	C	C	C	C	C	C	C	A	A	GT	CG
247	C	A	A	A	A	A	A	A	T	T	GT	CG
248	A	C	C	C	C	C	A	A	G	G	GG	CG
249	C	A	A	A	A	A	A	A	G	G	GG	CG
250	A	T	T	T	T	T	A	A	T	T	GG	CG
251	T	G	T	G	T	G	T	T	G	T	GG	CG
252	G	G	G	G	G	G	G	G	G	G	GG	CG
253	G	G	G	G	G	G	G	G	G	G	GG	CG
254	G	G	G	G	G	G	G	G	G	G	GG	CG
255	G	G	G	G	G	G	G	G	G	G	GG	CG
256	G	G	G	G	G	G	G	G	G	G	GG	CG
257	G	G	G	G	G	G	G	G	G	G	GG	CG
258	G	G	G	G	G	G	G	G	G	G	GG	CG
259	G	G	G	G	G	G	G	G	G	G	GG	CG
260	G	G	G	G	G	G	G	G	G	G	GG	CG
261	T	A	C	T	A	C	T	T	T	T	GG	CG
262	A	C	T	A	C	T	C	C	C	C	GG	CG
263	C	T	C	A	A	A	A	A	A	A	GG	CG
264	A	A	A	A	A	A	A	A	A	A	GG	CG
265	A	A	A	A	A	A	A	A	A	A	GG	CG
266	A	A	A	A	A	A	A	A	A	A	GG	CG
267	A	G	G	G	G	G	G	G	G	G	GG	CG
268	G	C	C	C	C	C	C	C	C	C	GG	CG
269	C	C	C	C	C	C	C	C	C	C	GG	CG
270	C	A	A	A	A	A	A	A	A	A	GG	CG
271	A	A	A	A	A	A	A	A	A	A	GG	CG
272	A	G	G	G	G	G	G	G	G	G	GG	CG
273	G	C	T	T	G	T	G	G	G	G	GG	CG
274	C	T	G	A	A	A	A	A	A	A	GG	CG
275	T	G	A	A	A	A	A	A	A	A	GG	CG
276	G	A	A	A	A	A	A	A	A	A	GG	CG
277	A	G	G	G	G	G	G	G	G	G	GG	CG
278	G	C	C	C	C	C	C	C	C	C	GG	CG
279	C	A	A	A	A	A	A	A	A	A	GG	CG
280	A	G	G	G	G	G	G	G	G	G	GG	CG
281	T	G	T	G	T	G	T	G	T	G	GG	CG
282	G	T	G	T	G	T	G	T	G	T	GG	CG
283	T	G	T	G	T	G	T	G	T	G	GG	CG
284	G	C	C	C	C	C	C	C	C	C	GG	CG
285	C	A	A	A	A	A	A	A	A	A	GG	CG
286	A	G	G	G	G	G	G	G	G	G	GG	CG
287	G	C	C	C	C	C	C	C	C	C	GG	CG
288	C	A	A	A	A	A	A	A	A	A	GG	CG
289	A	G	G	G	G	G	G	G	G	G	GG	CG
290	G	C	C	C	C	C	C	C	C	C	GG	CG
291	C	A	A	A	A	A	A	A	A	A	GG	CG
292	A	G	G	G	G	G	G	G	G	G	GG	CG
293	G	C	C	C	C	C	C	C	C	C	GG	CG
294	A	G	G	G	G	G	G	G	G	G	GG	CG
295	C	G	A	A	A	A	A	A	A	A	GG	CG
296	G	C	G	A	A	A	A	A	A	A	GG	CG
297	A	A	G	A	A	A	A	A	A	A	GG	CG
298	A	A	G	A	A	A	A	A	A	A	GG	CG
299	A	A	G	A	A	A	A	A	A	A	GG	CG
300	A	A	G	A	A	A	A	A	A	A	GG	CG
301	A	A	G	A	A	A	A	A	A	A	GG	CG
302	A	G	A	G	A	A	A	A	A	A	GG	CG
303	G	T	G	T	G	T	G	T	G	T	GG	CG
304	T	G	T	G	T	G	T	G	T	G	GG	CG
305	G	T	G	T	G	T	G	T	G	T	GG	CG
306	T	G	T	G	T	G	T	G	T	G	GG	CG
307	G	A	C	A	C	A	A	A	A	A	GG	CG
308	A	C	A	C	A	A	A	A	A	A	GG	CG
309	C	A	A	A	A	A	A	A	A	A	GG	CG
310	A	A	A	A	A	A	A	A	A	A	GG	CG
311	A	A	A	A	A	A	A	A	A	A	GG	CG
312	A	G	A	G	A	A	A	A	A	A	GG	CG
313	G	T	C	G	T	G	C	A	A	A	GG	CG
314	T	C	G	T	G	C	A	A	A	A	GG	CG
315	C	G	T	G	C	A	A	A	A	A	GG	CG
316	G	T	G	C	A	A	A	A	A	A	GG	CG
317	T	G	C	A	A	A	A	A	A	A	GG	CG
318	G	C	A	G	A	A	A	A	A	A	GG	CG
319	C	A	G	A	G	A	A	A	A	A	GG	CG
320	A	G	A	G	A	G	A	A	A	A	GG	CG
321	G	A	A	G	A	G	A	A	A	A	GG	CG
322	A	A	A	G	A	G	A	A	A	A	GG	CG
323	A	A	A	G	A	G	A	A	A	A	GG	CG
324	A	A	A	G	A	G	A	A	A	A	GG	CG
325	A	A	A	G	A	G	A	A	A	A	GG	CG
326	A	A	A	G	A	G	A	A	A	A	GG	CG
327	A	A	A	G	A	G	A	A	A	A	GG	CG
328	A	A	A	G	A	G	A	A	A	A	GG	CG
329	A	A	A	G	A	G	A	A	A	A	GG	CG
330	A	A	A	G	A	G	A	A	A	A	GG	CG
331	A	A	A	G	A	G	A	A	A	A	GG	CG
332	A	A	A	G	A	G	A	A	A	A	GG	CG
333	A	A	A	G	A	G	A	A	A	A	GG	CG
334	A	A	A	G	A	G	A	A	A	A	GG	CG
335	A	A	A	G	A	G	A	A	A	A	GG	CG
336	A	A	A	G	A	G	A	A	A	A	GG	CG
337	A	A	A	G	A	G	A	A	A	A	GG	CG
338	A	A	A	G	A	G	A	A	A	A	GG	CG
339	A	A	A	G	A	G	A	A	A	A	GG	CG
340	A	A	A	G	A	G	A	A	A	A	GG	CG
341	A	A	A	G	A	G	A	A	A	A	GG	CG
342	A	A	A	G	A	G	A	A	A	A	GG	CG
343	A	A	A	G	A	G	A	A	A	A	GG	CG
344	A	A	A	G	A	G	A	A	A	A	GG	CG
345	A	A	A	G	A	G	A	A	A	A	GG	CG
346	A	A	A	G	A	G	A	A	A	A	GG	CG
347	A	A	A	G	A	G	A	A	A	A	GG	CG
348	A	A	A	G	A	G	A	A	A	A	GG	CG
349	A	A	A	G	A	G	A	A	A	A	GG	CG
350	A	A	A	G	A	G	A	A	A	A	GG	CG
351	A	A	A	G	A	G	A	A	A	A	GG	CG
352	A	A	A	G	A	G	A	A	A	A	GG	CG
353	A	A	A	G	A	G	A	A	A	A	GG	CG

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm 13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	C	C	C	C	G	N	C	N	T	N
356	C	C	G	G	G	G	G	G	G	G	C	G
357	G	G	G	G	G	G	G	G	G	N	N	N
358	G	G	G	G	G	G	G	G	G	N	N	N
359	G	G	G	G	G	G	G	G	G	N	N	N
360	T	T	T	T	T	T	T	T	T	N	N	R
361	T	T	T	T	T	T	T	T	T	R	N	R
362	A	A	A	A	A	A	A	A	A	N	N	N
363	T	T	T	T	T	T	T	T	T	N	N	R
364	T	T	T	T	T	T	T	T	T	R	N	R
365	A	A	A	A	A	A	A	A	A	N	N	N
366	C	C	C	C	C	C	C	C	C	N	N	N
367	A	A	A	A	A	A	A	A	A	N	N	N
368	C	C	C	C	C	C	C	C	C	N	N	N
369	C	C	C	C	C	C	C	C	C	N	N	N
370	T	T	T	T	T	T	T	T	T	T	A	T
371	T	T	T	T	T	T	T	T	T	T	A	T
372	C	C	C	C	C	C	C	C	C	T	A	T
373	A	A	A	A	A	A	A	A	A	A	A	A
374	G	G	G	G	G	G	G	G	G	G	G	G
375	T	T	T	T	T	T	T	T	T	T	T	T
376	G	G	G	G	G	G	G	G	G	G	G	G
377	T	T	T	T	T	T	T	T	T	T	T	T
378	T	T	T	T	T	T	T	T	T	T	T	T
379	A	A	A	A	A	A	A	A	A	A	A	A
380	T	T	T	T	T	T	T	T	T	T	T	T
381	T	T	T	T	T	T	T	T	T	T	T	T
382	A	A	A	A	A	A	A	A	A	A	A	A
383	C	C	C	C	C	C	C	C	C	C	C	C
384	G	G	G	G	G	G	G	G	G	G	G	G
385	A	A	A	A	A	A	A	A	A	A	A	A
386	C	C	C	C	C	C	C	C	C	C	C	C
387	C	C	C	C	C	C	C	C	C	C	C	C
388	G	G	G	G	G	G	G	G	G	G	G	G
389	A	A	A	A	A	A	A	A	A	A	A	A
390	C	C	C	C	C	C	C	C	C	C	C	C
391	A	A	A	A	A	A	A	A	A	A	A	A
392	A	A	A	A	A	A	A	A	A	A	A	A
393	A	A	A	A	A	A	A	A	A	A	A	A
394	C	C	C	C	C	C	C	C	C	C	C	C
395	C	C	C	C	C	C	C	C	C	C	C	C
396	T	T	T	T	T	T	T	T	T	T	T	T
397	G	G	G	G	G	G	G	G	G	G	G	G
398	A	A	A	A	A	A	A	A	A	A	A	A
399	T	T	T	T	T	T	T	T	T	T	T	T
400	T	T	T	T	T	T	T	T	T	T	T	T
401	C	C	C	C	C	C	C	C	C	C	C	C
402	T	T	T	T	T	T	T	T	T	T	T	T
403	T	T	T	T	T	T	T	T	T	T	T	T
404	C	C	C	C	C	C	C	C	C	C	C	C
405	T	T	T	T	T	T	T	T	T	T	T	T
406	T	T	T	T	T	T	T	T	T	T	T	T
407	C	C	C	C	C	C	C	C	C	C	C	C
408	T	T	T	T	T	T	T	T	T	T	T	T
409	T	T	T	T	T	T	T	T	T	T	T	T
410	A	A	A	A	A	A	A	A	A	A	A	A
411	A	A	A	A	A	A	A	A	A	A	A	A
412	T	T	T	T	T	T	T	T	T	T	T	T
413	T	T	T	T	T	T	T	T	T	T	T	T
414	C	C	C	C	C	C	C	C	C	C	C	C
415	T	T	T	T	T	T	T	T	T	T	T	T
416	T	T	T	T	T	T	T	T	T	T	T	T
417	G	G	G	G	G	G	G	G	G	G	G	G
418	A	A	A	A	A	A	A	A	A	A	A	A
419	T	T	T	T	T	T	T	T	T	T	T	T
420	A	A	A	A	A	A	A	A	A	A	A	A
421	T	T	T	T	T	T	T	T	T	T	T	T
422	T	T	T	T	T	T	T	T	T	T	T	T
423	T	T	T	T	T	T	T	T	T	T	T	T
424	T	T	T	T	T	T	T	T	T	T	T	T
425	T	T	T	T	T	T	T	T	T	T	T	T
426	G	G	G	G	G	G	G	G	G	G	G	G
427	A	A	A	A	A	A	A	A	A	A	A	A
428	T	T	T	T	T	T	T	T	T	T	T	T
429	T	T	T	T	T	T	T	T	T	T	T	T
430	T	T	T	T	T	T	T	T	T	T	T	T
431	T	T	T	T	T	T	T	T	T	T	T	T
432	A	A	A	A	A	A	A	A	A	A	A	A
433	A	A	A	A	A	A	A	A	A	A	A	A
434	C	C	C	C	C	C	C	C	C	C	C	C
435	C	C	C	C	C	C	C	C	C	C	C	C
436	C	C	C	C	C	C	C	C	C	C	C	C
437	T	T	T	T	T	T	T	T	T	T	T	T
438	T	T	T	T	T	T	T	T	T	T	T	T
439	A	A	A	A	A	A	A	A	A	A	A	A
440	A	A	A	A	A	A	A	A	A	A	A	A
441	A	A	A	A	A	A	A	A	A	A	A	A
442	A	A	A	A	A	A	A	A	A	A	A	A
443	A	A	A	A	A	A	A	A	A	A	A	A
444	A	A	A	A	A	A	A	A	A	A	A	A
445	A	A	A	A	A	A	A	A	A	A	A	A
446	G	G	G	G	G	G	G	G	G	G	G	G
447	A	A	A	A	A	A	A	A	A	A	A	A
448	T	T	T	T	T	T	T	T	T	T	T	T
449	T	T	T	T	T	T	T	T	T	T	T	T
450	T	T	T	T	T	T	T	T	T	T	T	T
451	T	T	T	T	T	T	T	T	T	T	T	T
452	T	T	T	T	T	T	T	T	T	T	T	T
453	T	T	T	T	T	T	T	T	T	T	T	T
454	T	T	T	T	T	T	T	T	T	T	T	T
455	T	T	T	T	T	T	T	T	T	T	T	T
456	T	T	T	T	T	T	T	T	T	T	T	T
457	T	T	T	T	T	T	T	T	T	T	T	T
458	T	T	T	T	T	T	T	T	T	T	T	T
459	T	T	T	T	T	T	T	T	T	T	T	T
460	T	T	T	T	T	T	T	T	T	T	T	T
461	T	T	T	T	T	T	T	T	T	T	T	T
462	T	T	T	T	T	T	T	T	T	T	T	T
463	T	T	T	T	T	T	T	T	T	T	T	T
464	T	T	T	T	T	T	T	T	T	T	T	T
465	T	T	T	T	T	T	T	T	T	T	T	T
466	T	T	T	T	T	T	T	T	T	T	T	T
467	T	T	T	T	T	T	T	T	T	T	T	T
468	T	T	T	T	T	T	T	T	T	T	T	T
469	T	T	T	T	T	T	T	T	T	T	T	T
470	T	T	T	T	T	T	T	T	T	T	T	T
471	T	T	T	T	T	T	T	T	T	T	T	T

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	APP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	T	N
479	G	G	G	G	G	G	G	G		T	T	N
480	T	T	T	T	T	T	T	N		N	A	N
481	A	A	C	A	C	A	T	Y		A	A	A
482	A	A	T	T	T	A	T	T		G	A	A
483	T	T	T	T	T	T	T	T		T	N	A
484	A	A	T	T	C	C	C	T		N	N	A
485	T	C	T	C	G	G	G	G		R	N	A
486	C	G	T	G	T	T	T	T		R	T	T
487	G	T	T	T	G	T	G	R		N	N	R
488	T	T	T	T	T	T	T	N		N	N	N
489	A	A	T	T	T	T	T	N		A	A	A
490	A	T	T	G	T	G	T	N		R	A	A
491	T	T	T	G	T	G	T	N		N	A	A
492	G	A	A	T	A	A	A	A		A	A	A
493	T	A	A	A	A	A	A	A		R	A	A
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
498	A	A	A	A	A	A	A	A		A	A	A
499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512	A	A	A	A	A	A	A	A		A	A	A

FIG. 7.2 Cont.

Position	Concession	Time	Concession	Time	Concession	Time
1	M	1m 12:44:22	M	1m 12:44:34	M	1m 12:44:49
2	K		K		K	
3	L		L		L	
4	L		L		L	
5	C		C		C	
6	C		C		C	
7	F		F		F	
8	F		F		F	
9	A		A		A	
10	A		A		A	
11	A		A		A	
12	A		A		A	
13	A		A		A	
14	A		A		A	
15	G		G		G	
16	G		G		G	
17	O		O		O	
18	O		O		O	
19	O		O		O	
20	O		O		O	
21	O		O		O	
22	O		O		O	
23	O		O		O	
24	O		O		O	
25	O		O		O	
26	O		O		O	
27	O		O		O	
28	O		O		O	
29	O		O		O	
30	O		O		O	
31	K		K		K	
32	K		K		K	
33	K		K		K	
34	K		K		K	
35	K		K		K	
36	K		K		K	
37	K		K		K	
38	K		K		K	
39	K		K		K	
40	G		G		G	
41	G		G		G	
42	G		G		G	
43	G		G		G	
44	G		G		G	
45	G		G		G	
46	G		G		G	
47	G		G		G	
48	G		G		G	
49	G		G		G	
50	G		G		G	
51	S		S		S	
52	S		S		S	
53	S		S		S	
54	S		S		S	
55	S		S		S	
56	S		S		S	
57	S		S		S	
58	S		S		S	
59	S		S		S	
60	S		S		S	
61	K		K		K	
62	K		K		K	
63	K		K		K	
64	K		K		K	
65	K		K		K	
66	K		K		K	
67	K		K		K	
68	K		K		K	
69	K		K		K	
70	K		K		K	
71	K		K		K	
72	K		K		K	
73	K		K		K	
74	K		K		K	
75	K		K		K	
76	K		K		K	
77	K		K		K	
78	K		K		K	
79	K		K		K	
80	K		K		K	
81	K		K		K	
82	K		K		K	
83	K		K		K	
84	K		K		K	
85	K		K		K	
86	K		K		K	
87	K		K		K	
88	K		K		K	
89	K		K		K	
90	K		K		K	
91	K		K		K	
92	K		K		K	
93	K		K		K	
94	K		K		K	
95	K		K		K	
96	K		K		K	
97	K		K		K	

FIG. 73

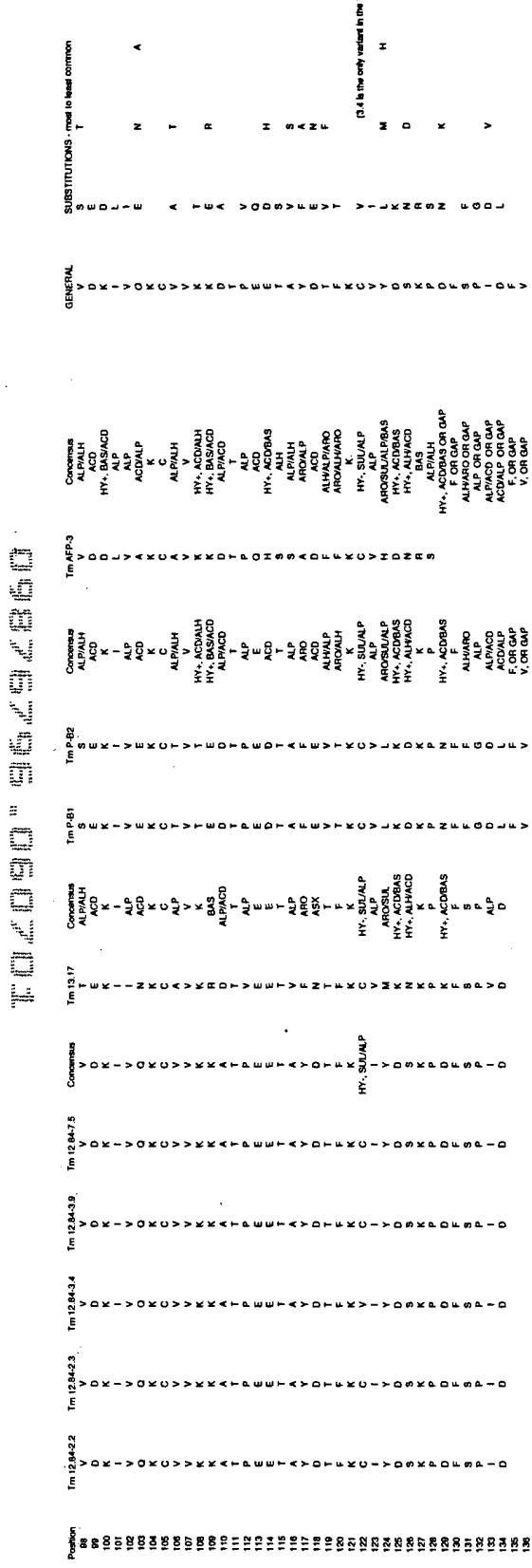


FIG. 7.3 Cont.

0987646 - 060201

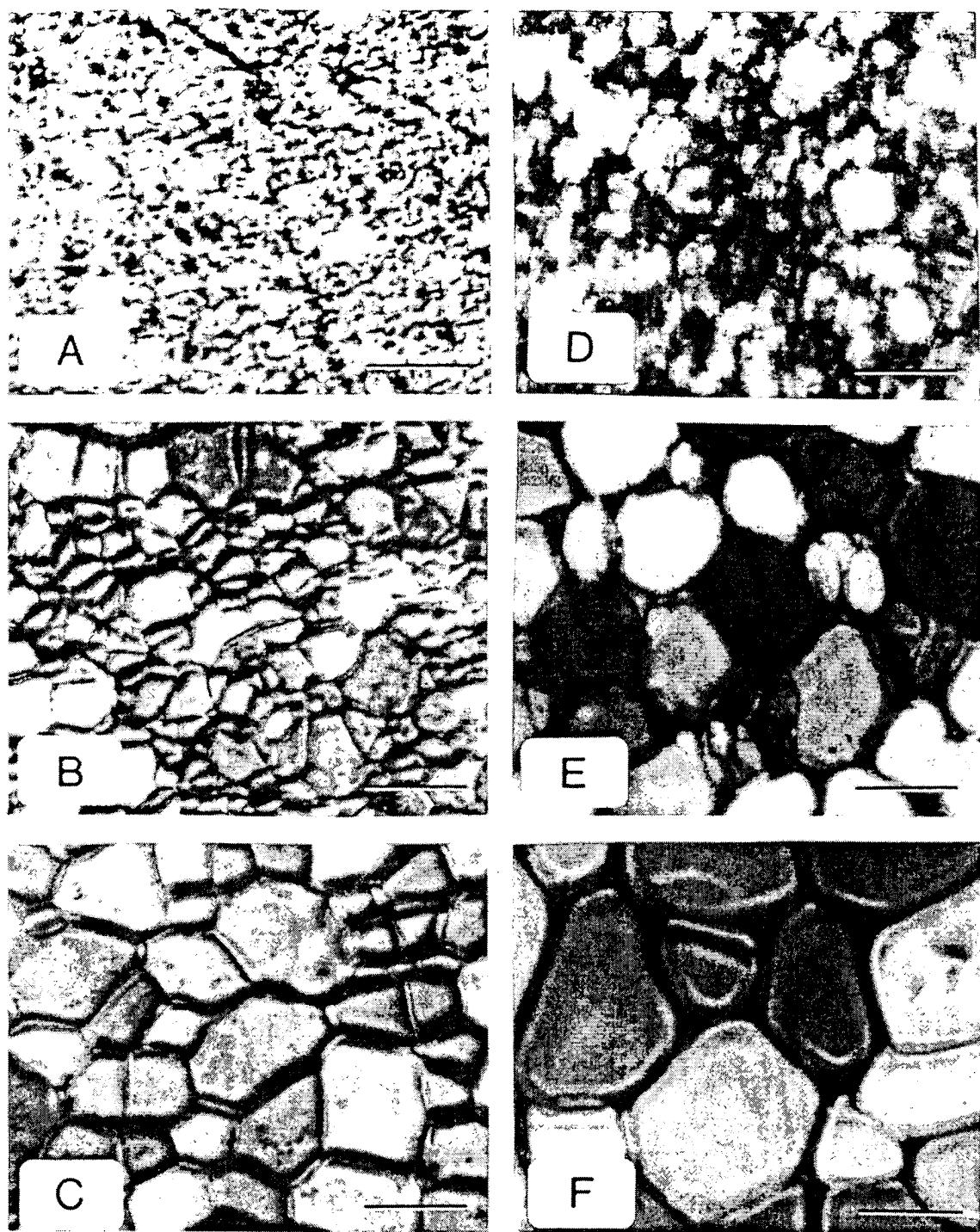


FIG. 8.0

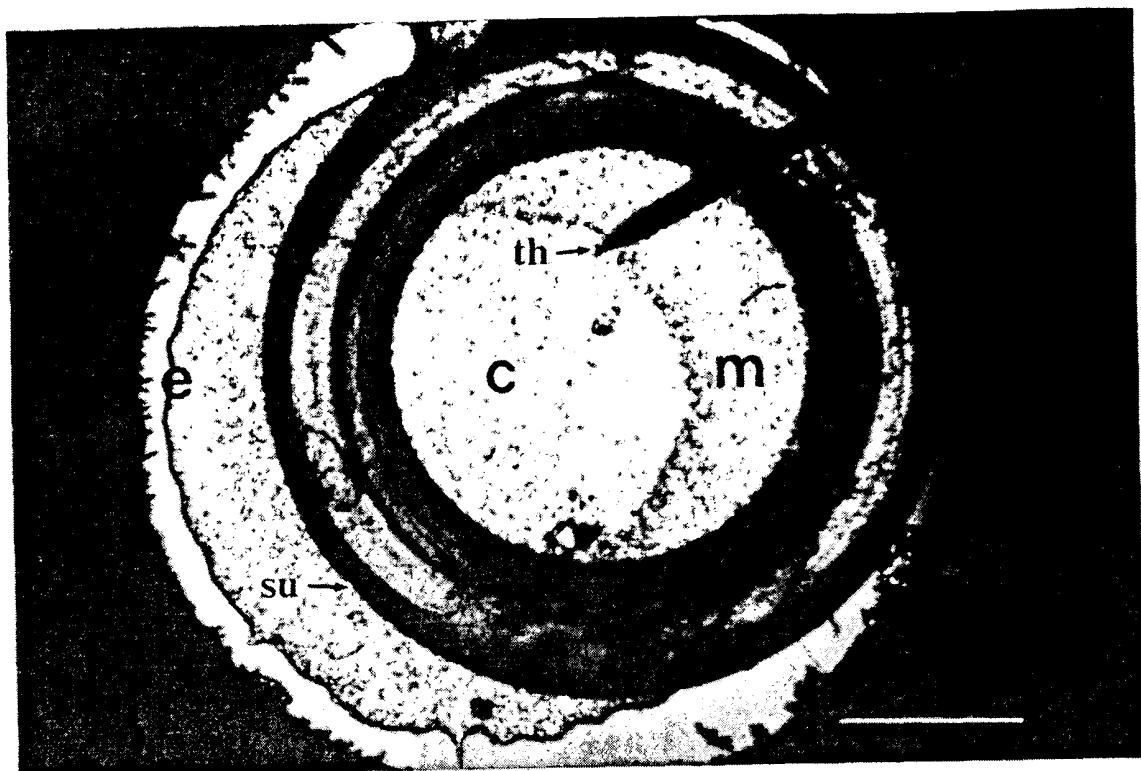


FIG. 8.1a

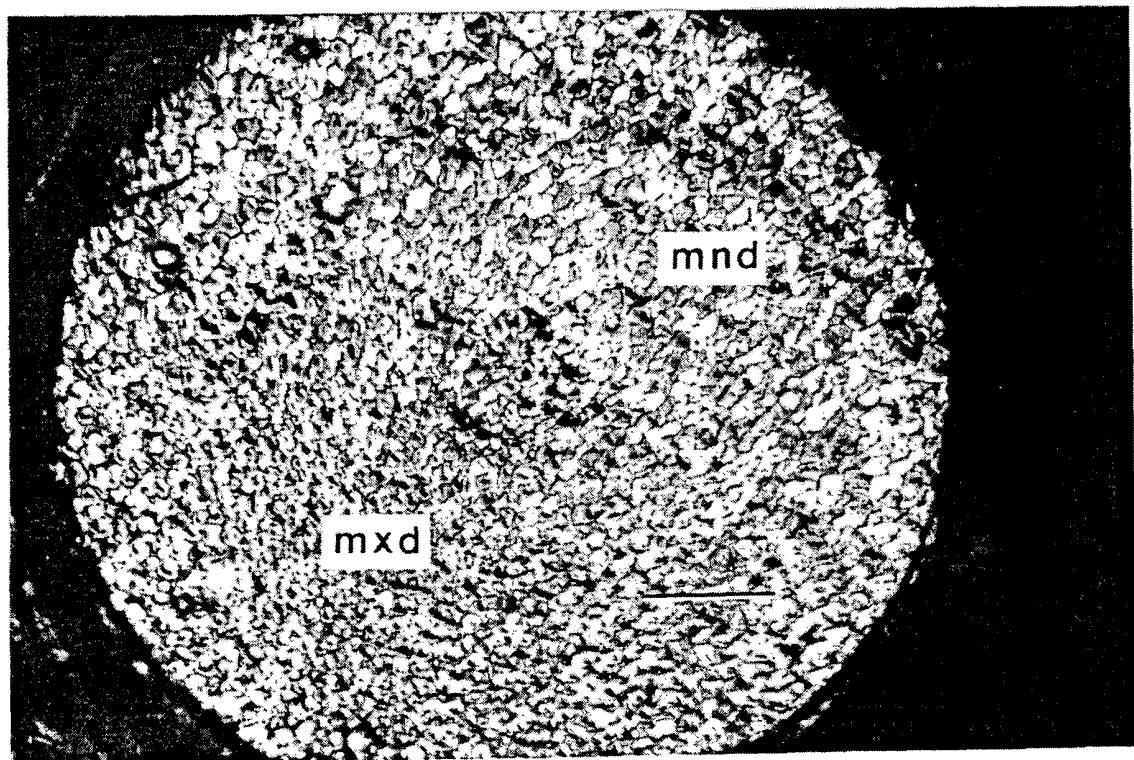
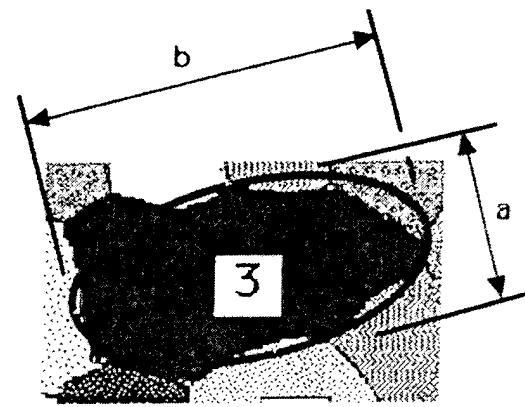
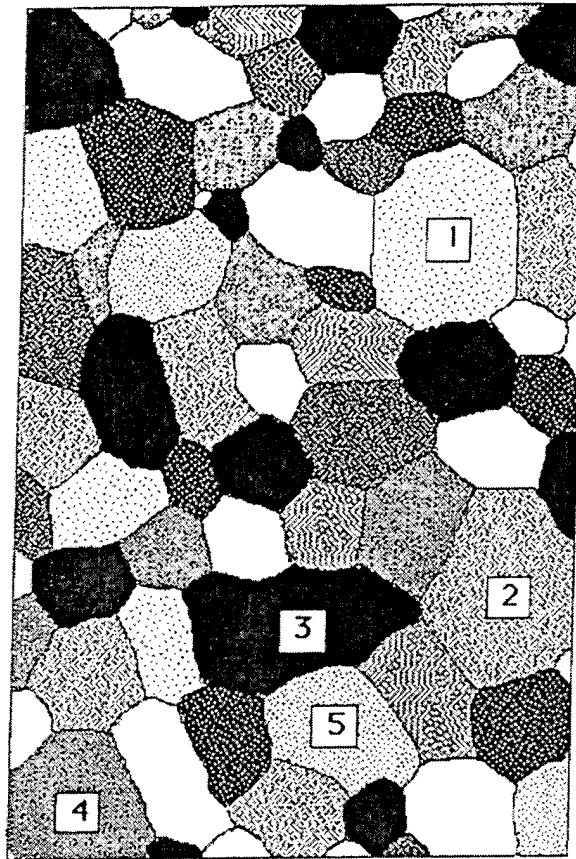


FIG. 8.1b



grain area=0.25mb

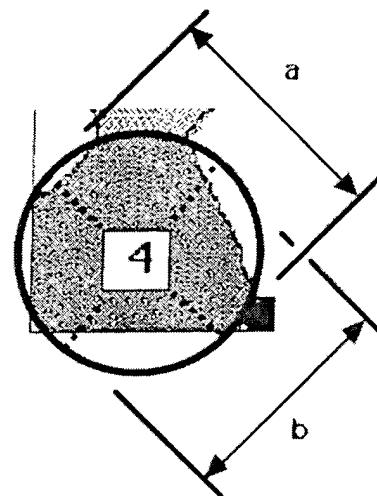


FIG. 8.2

098765432109876543210

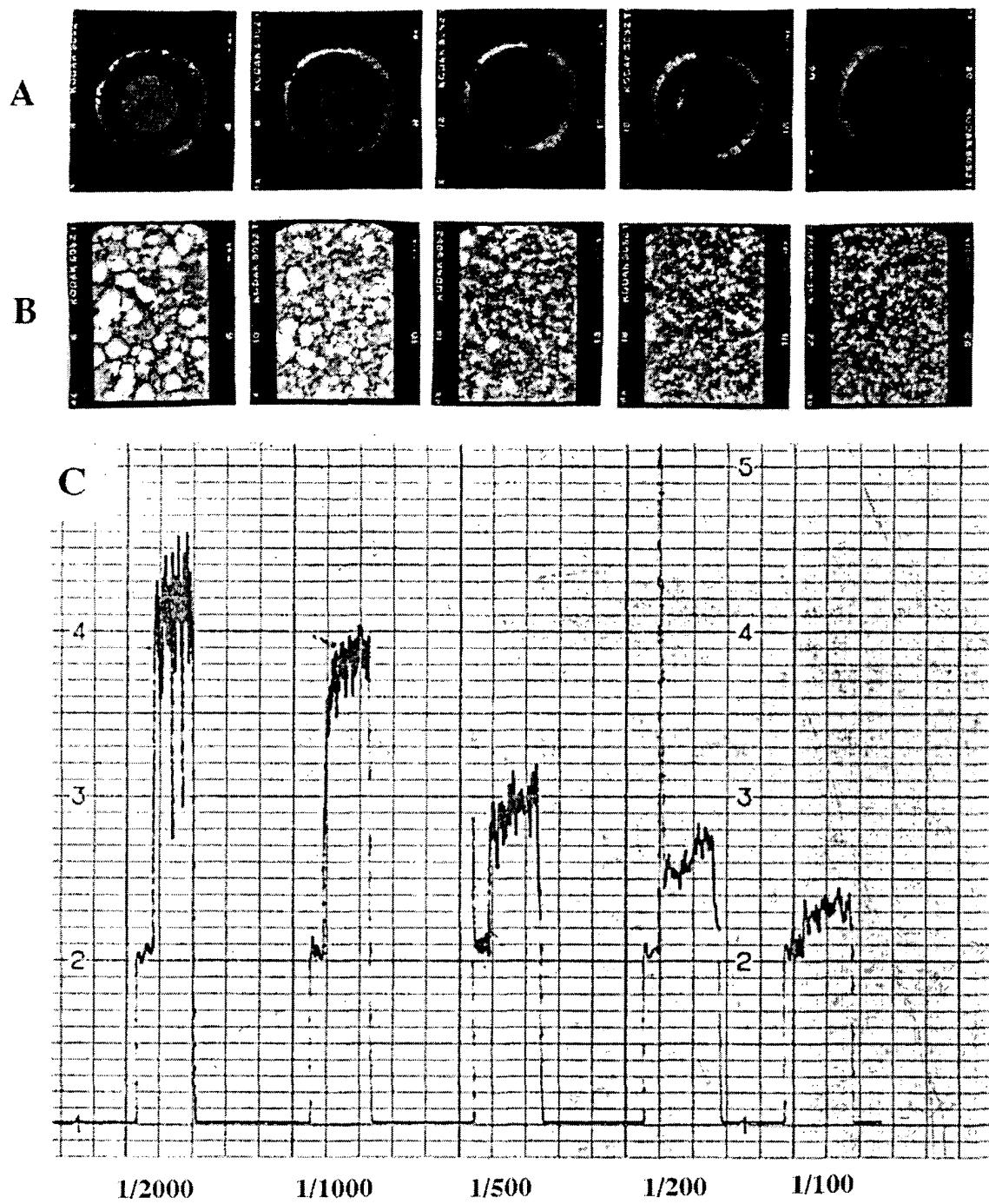


FIG. 8.3

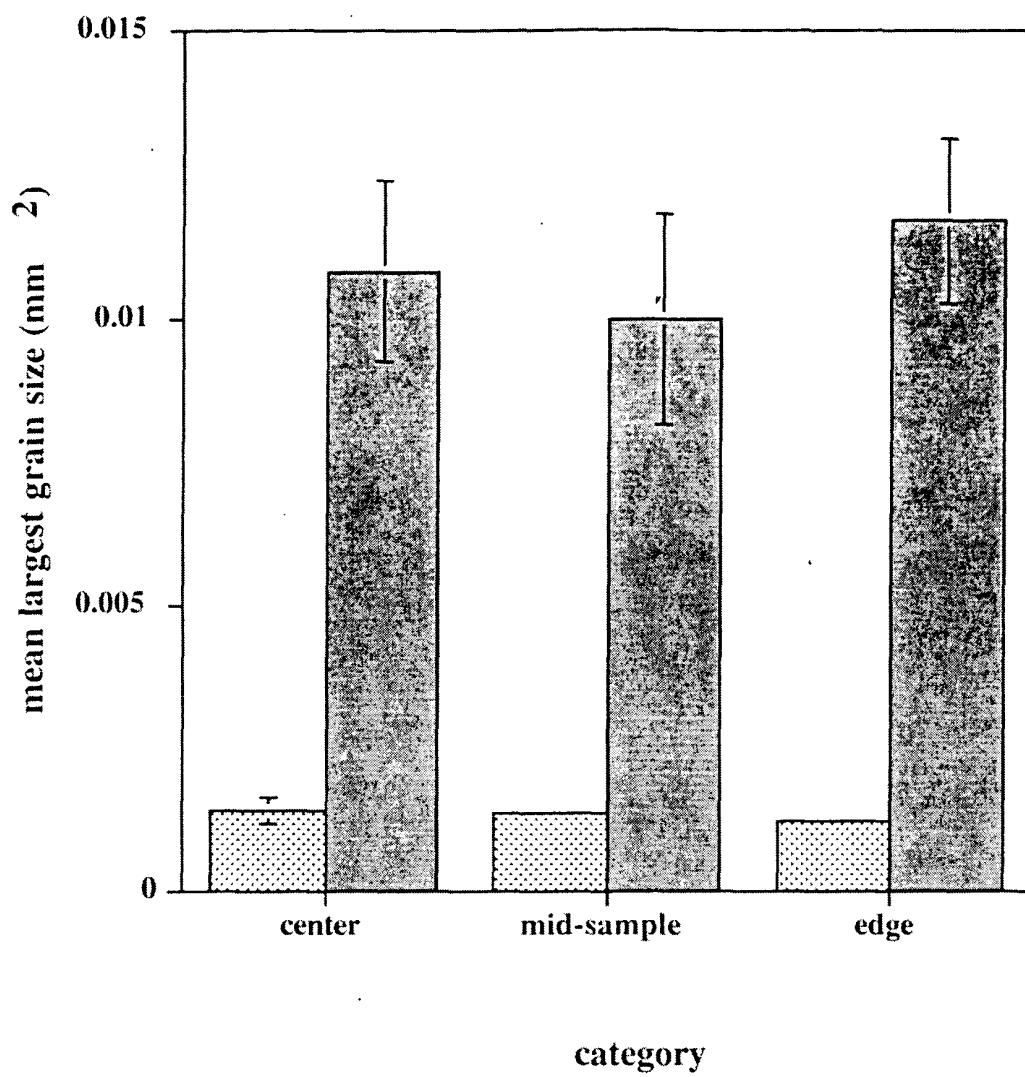


FIG. 8.4a

09876796-060204

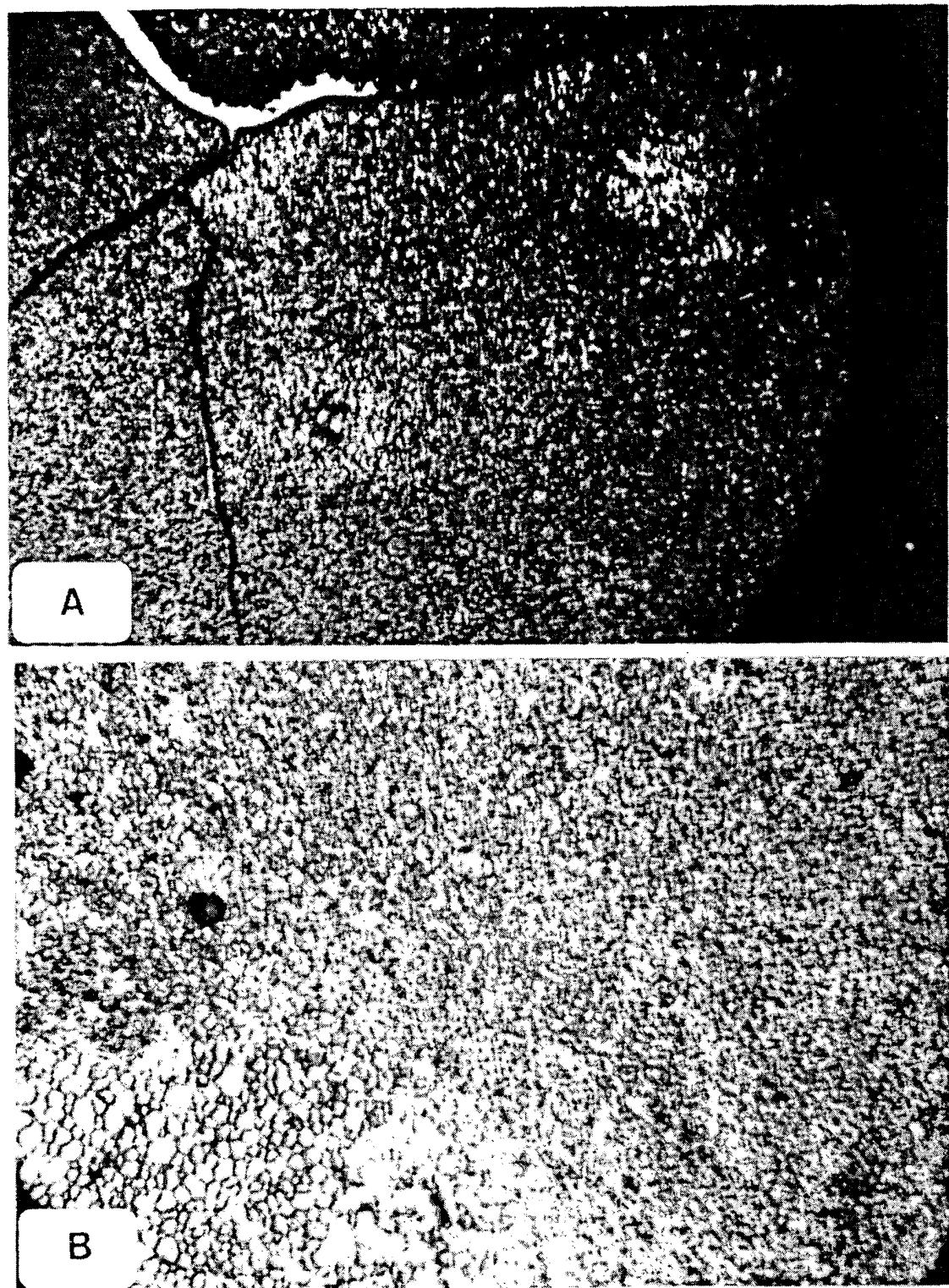


FIG. 8.4b

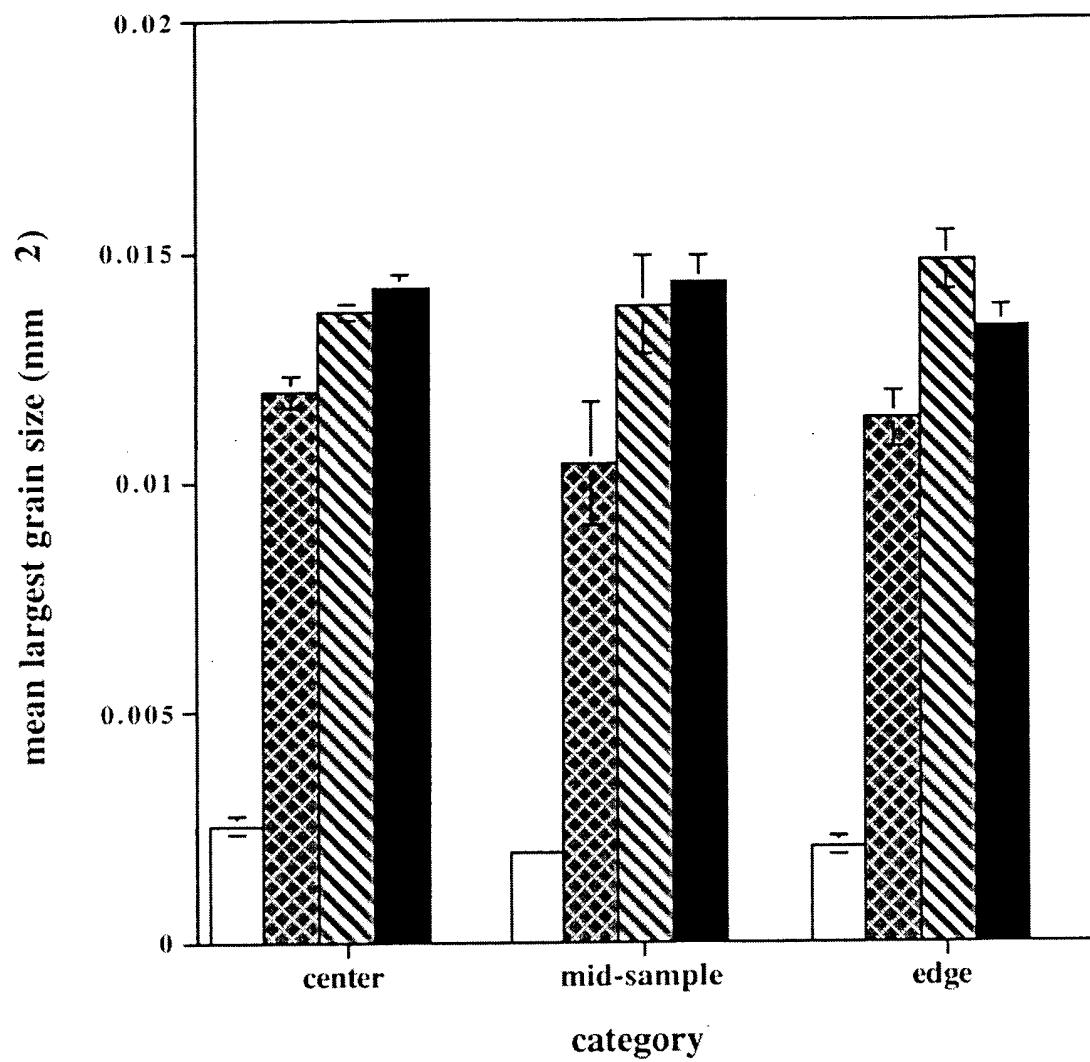


FIG. 8.5a

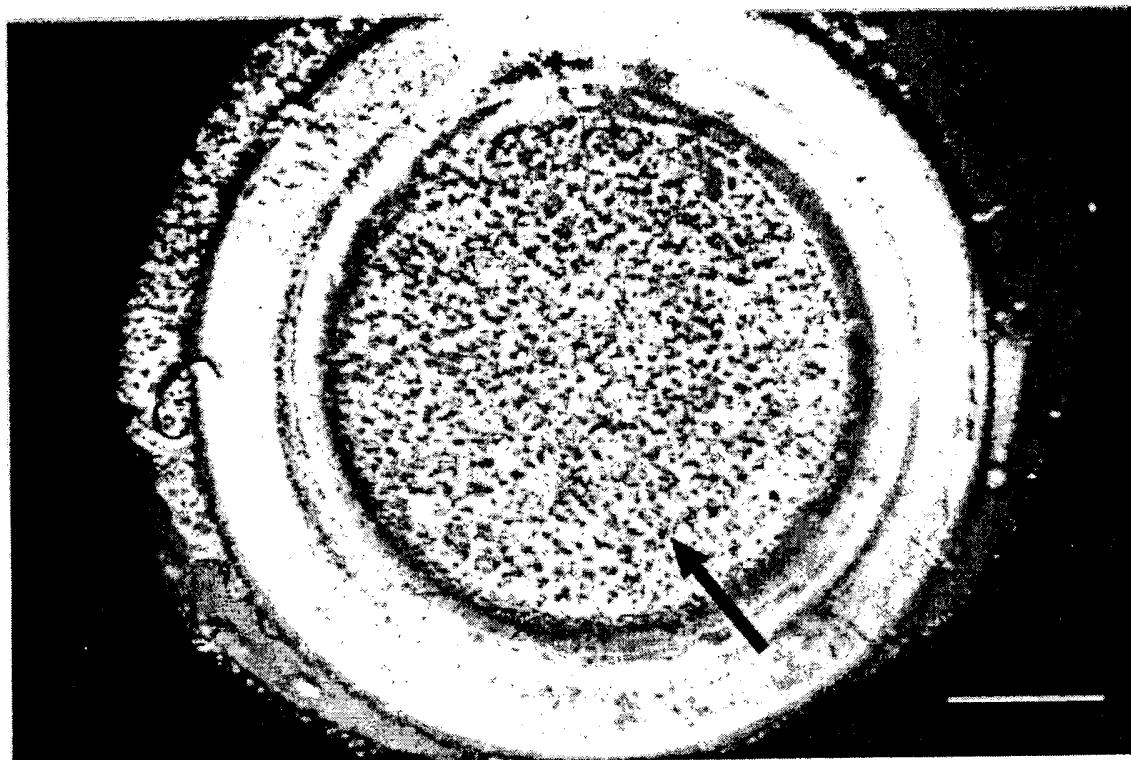


FIG. 8.5b

04926296 "060204

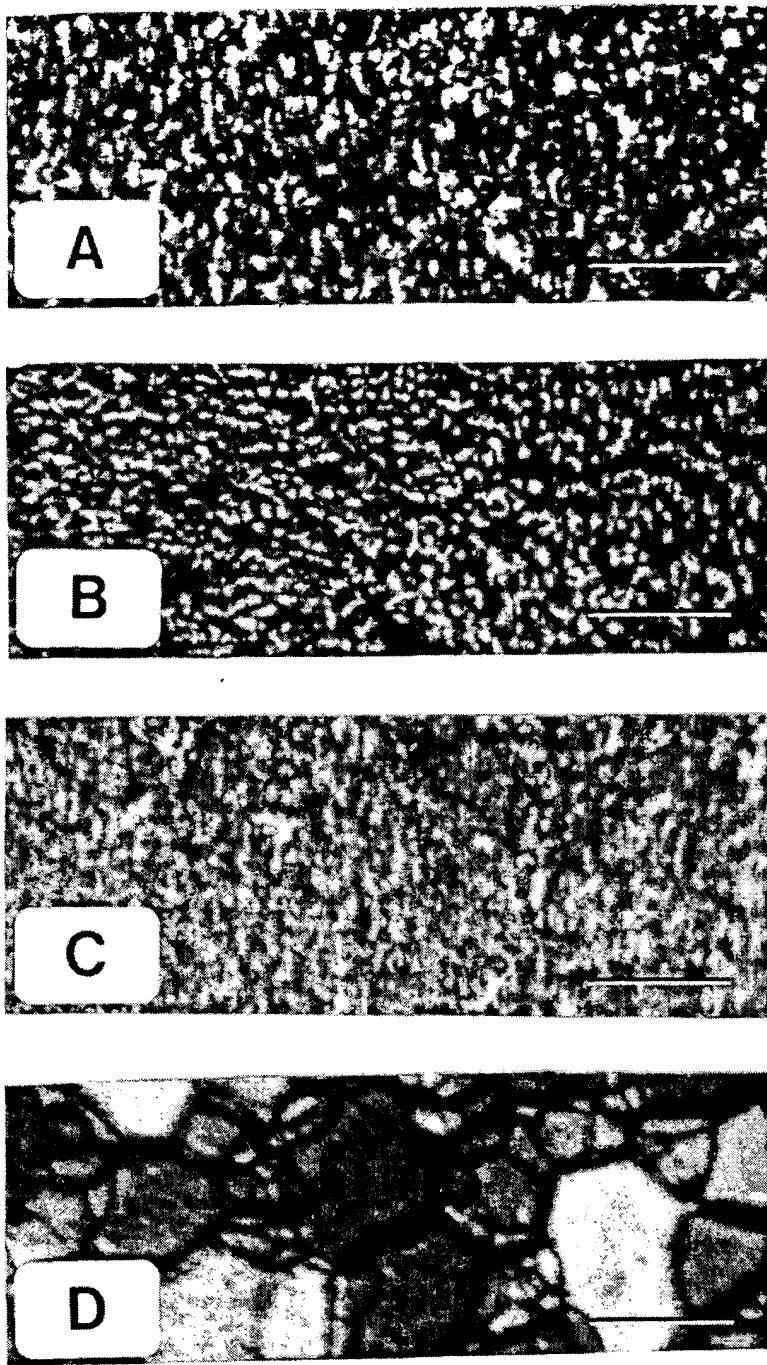


FIG. 8.6

FIGURE 8.7 96292860

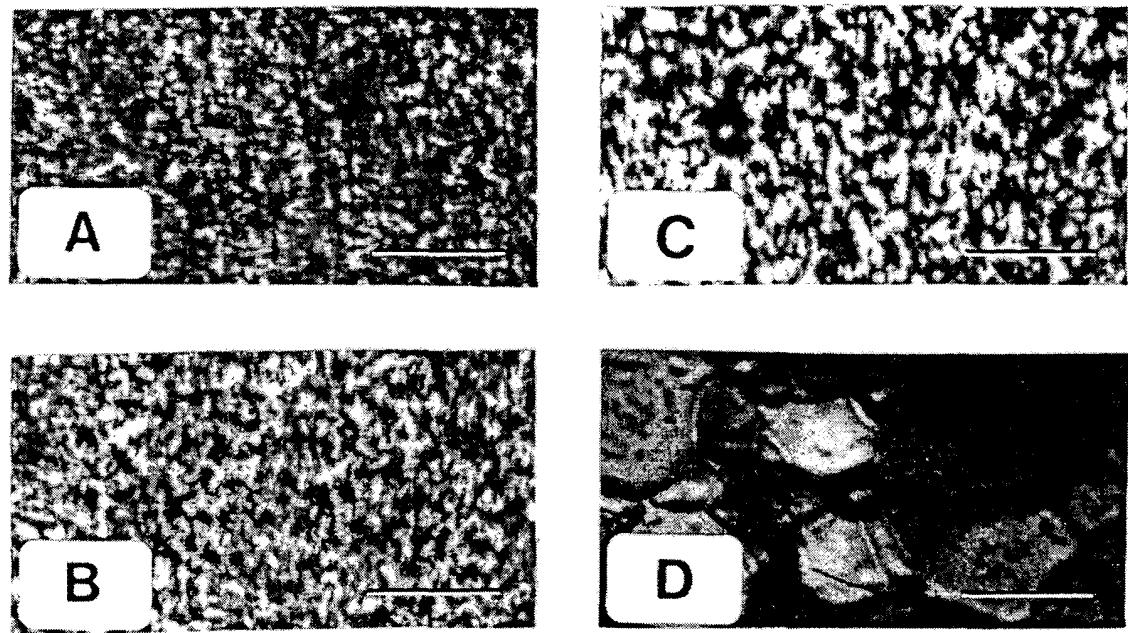


FIG. 8.7

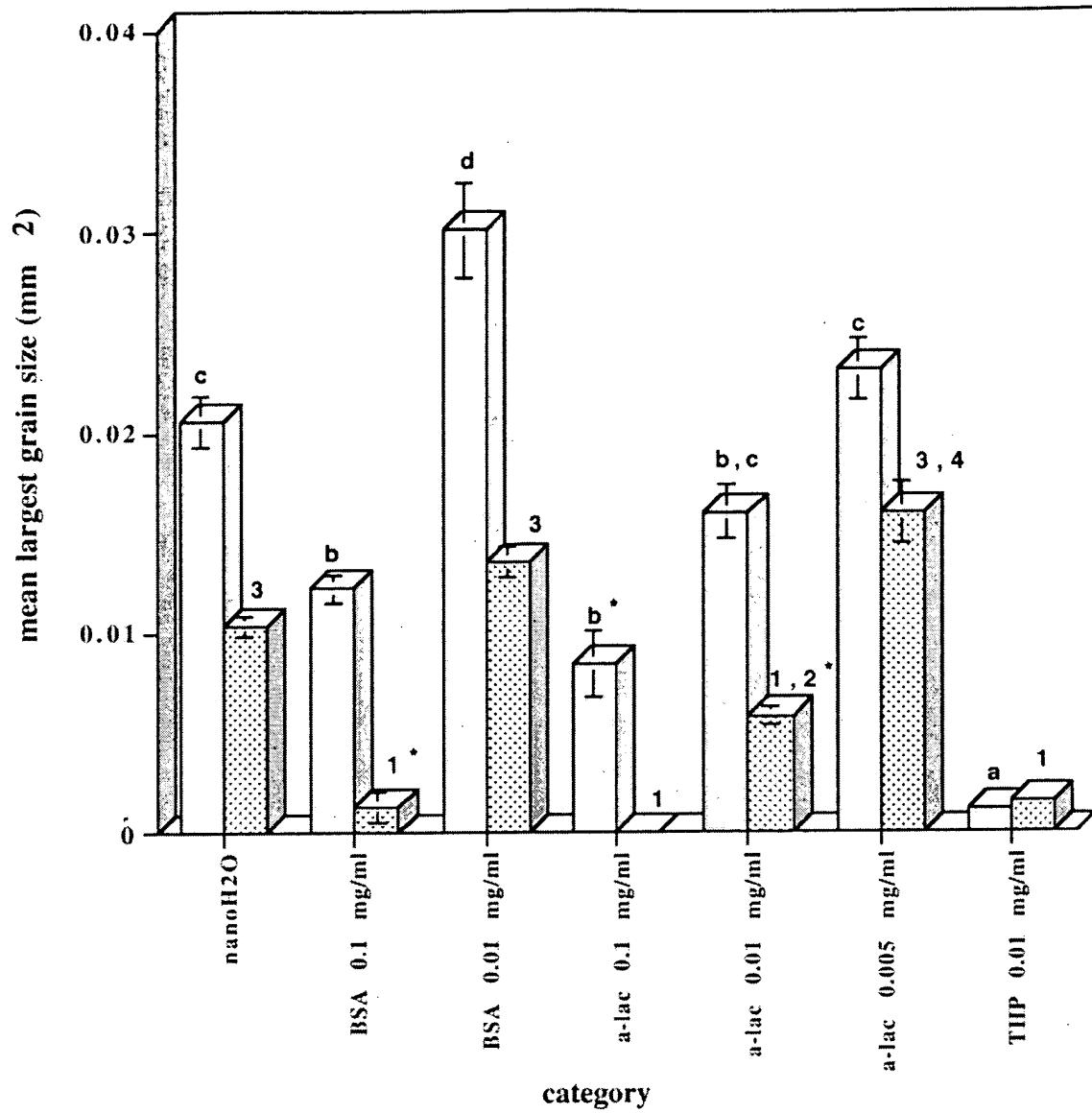


FIG. 8.8

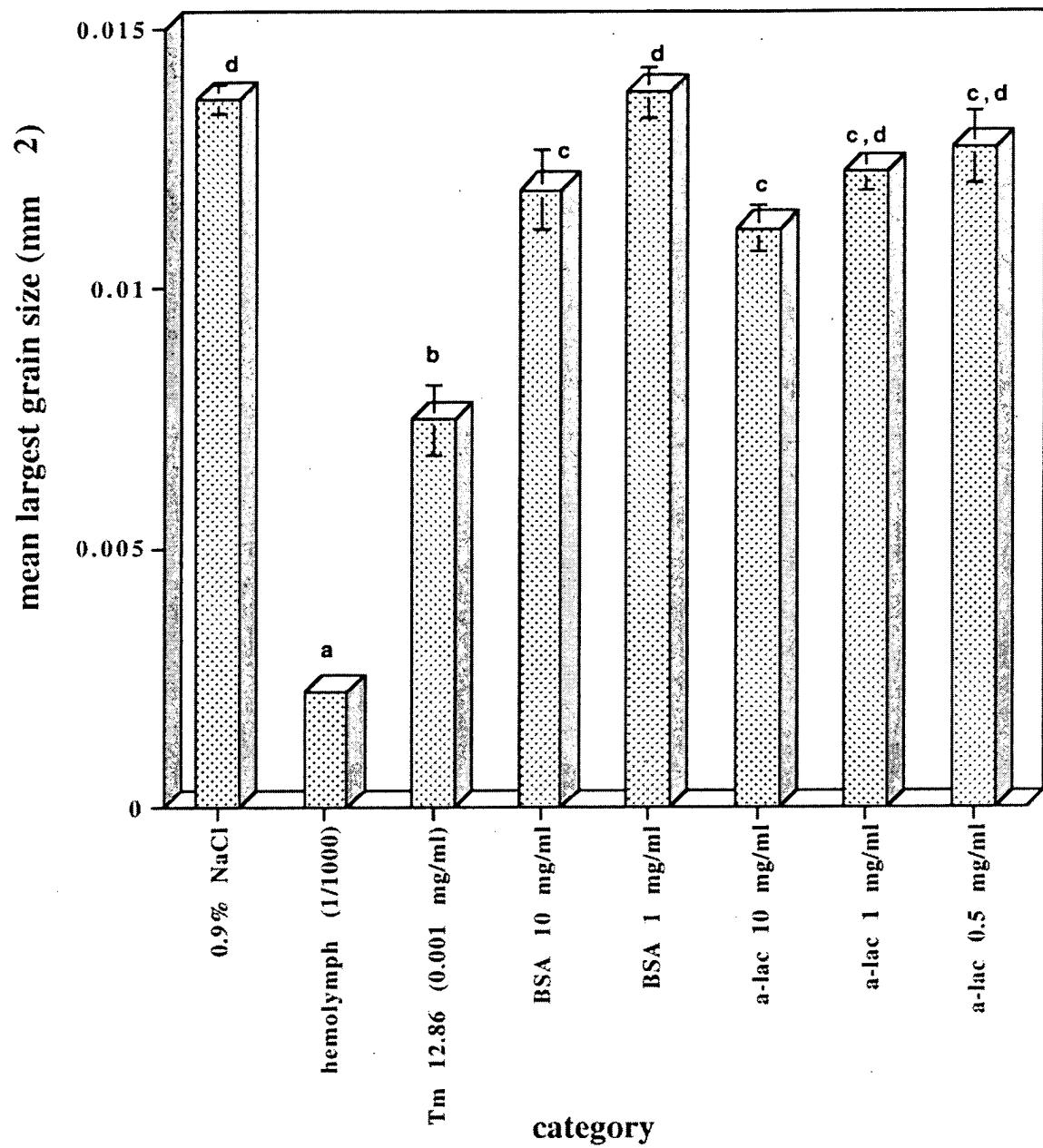


FIG. 8.9

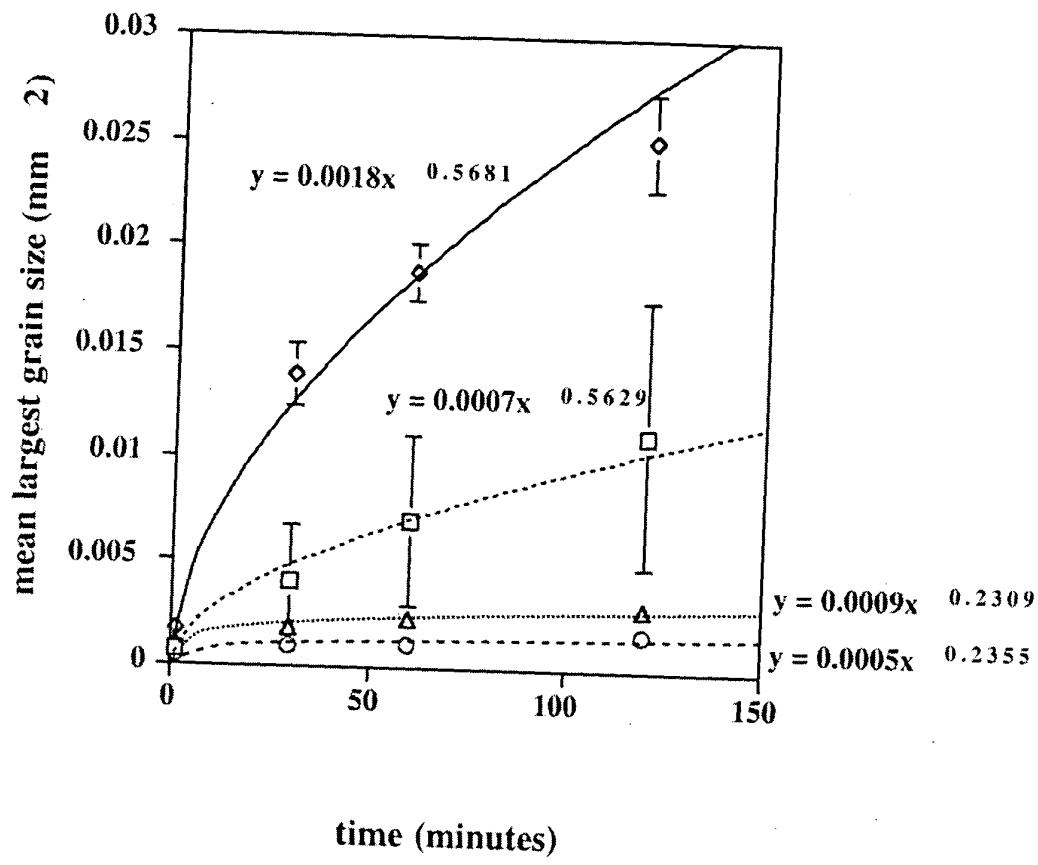


FIG. 8.10

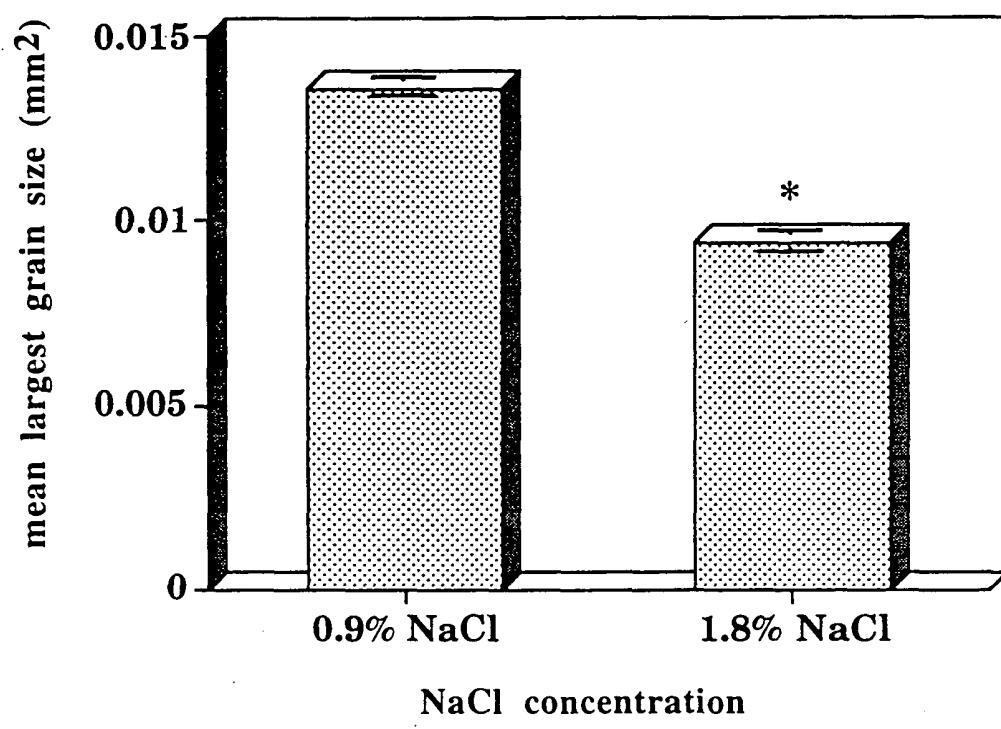


FIG. 8.11

09876543210

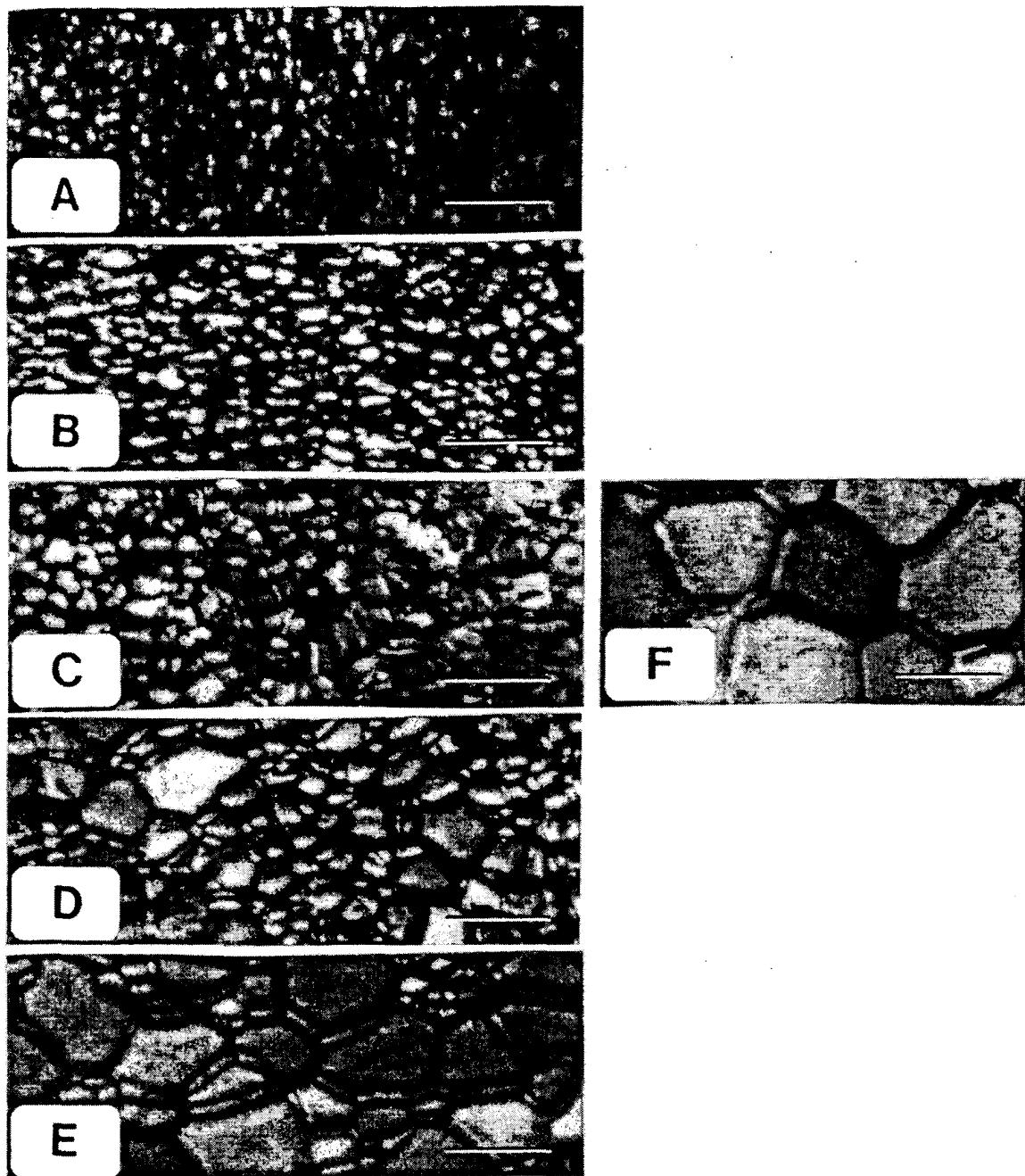


FIG. 8.12

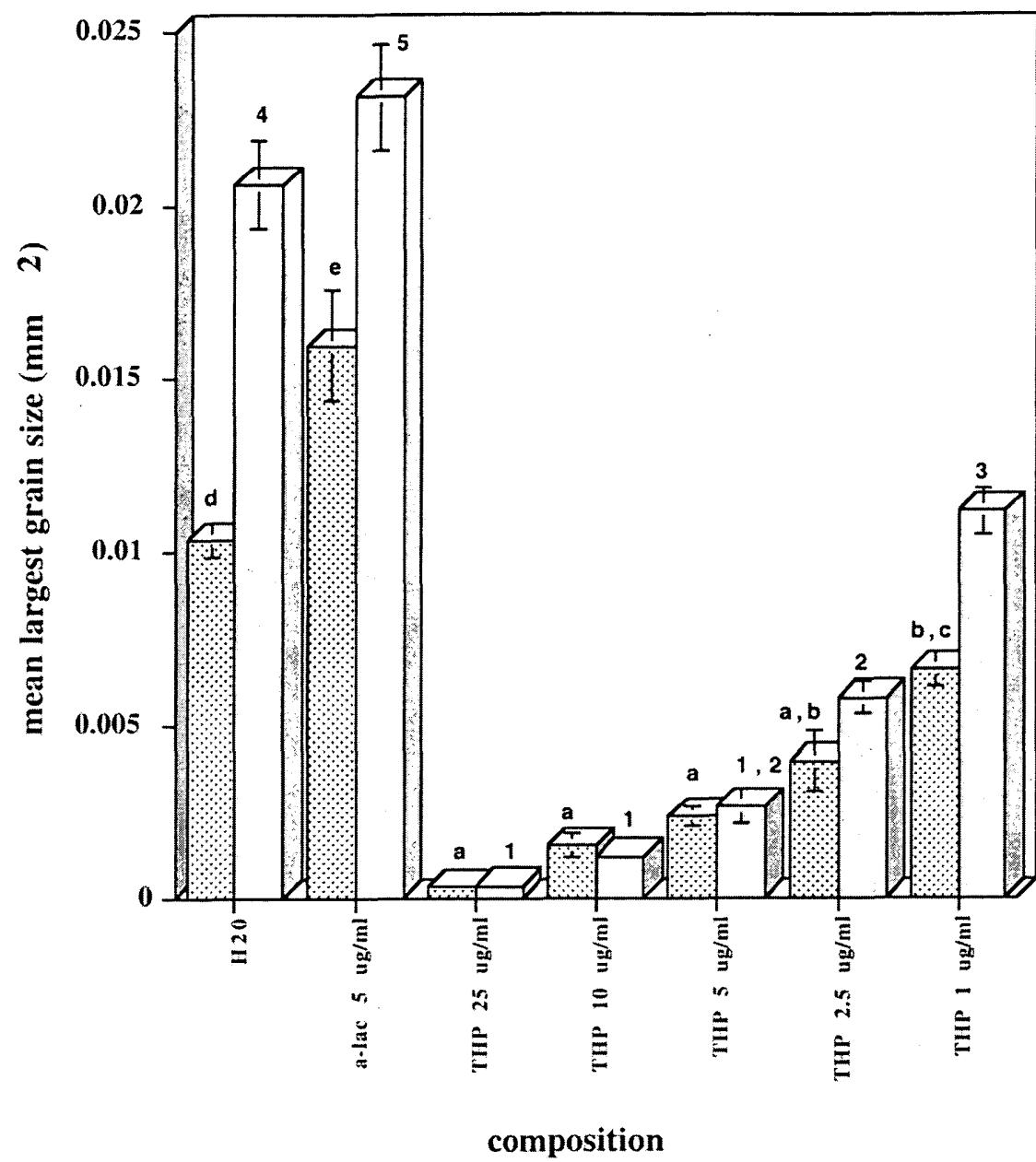


FIG. 8.13

0962262000-0226220200

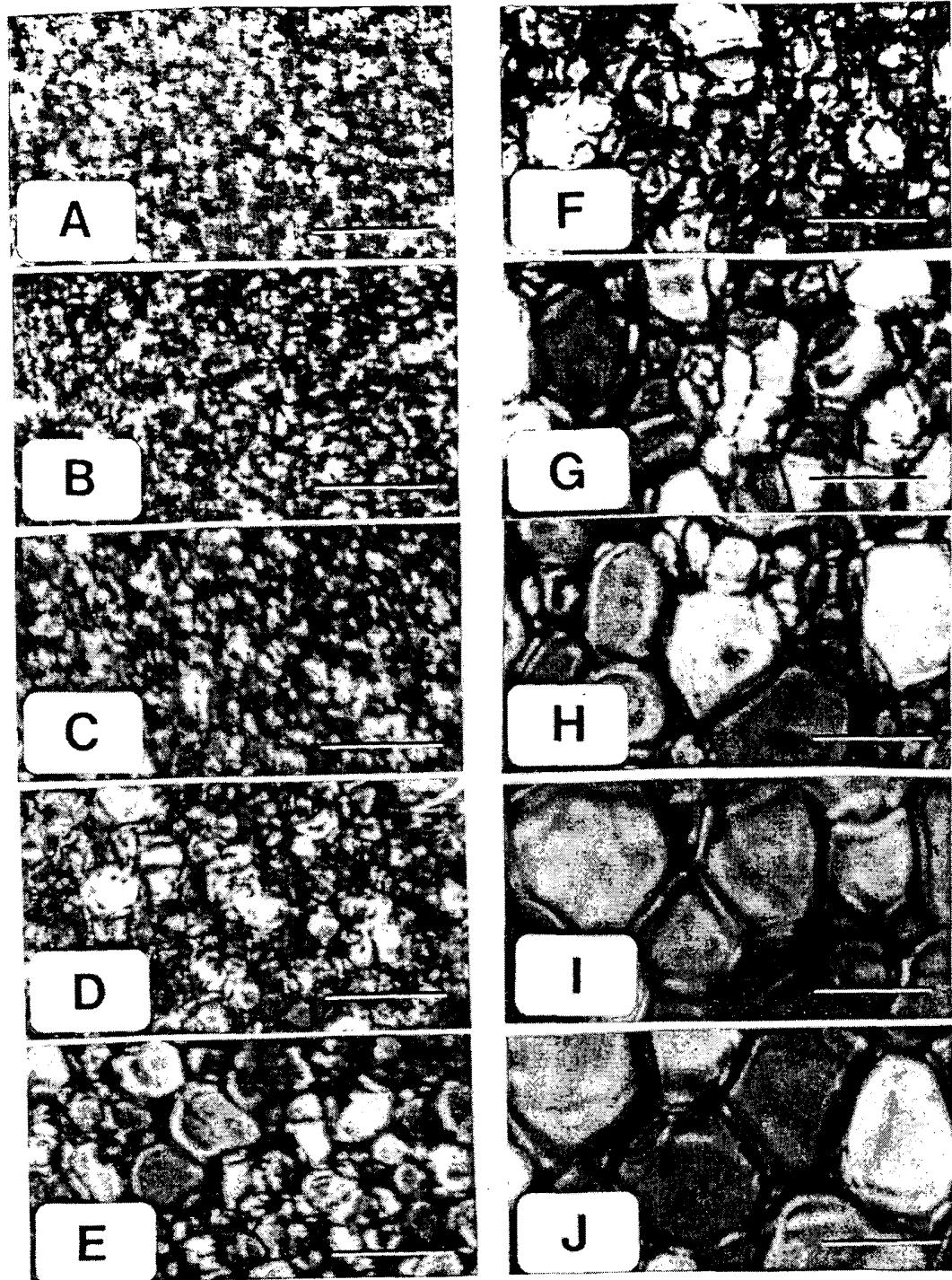


FIG. 8.14

mean largest grain size (mm^2)

■ -60 °C
□ -20 °C

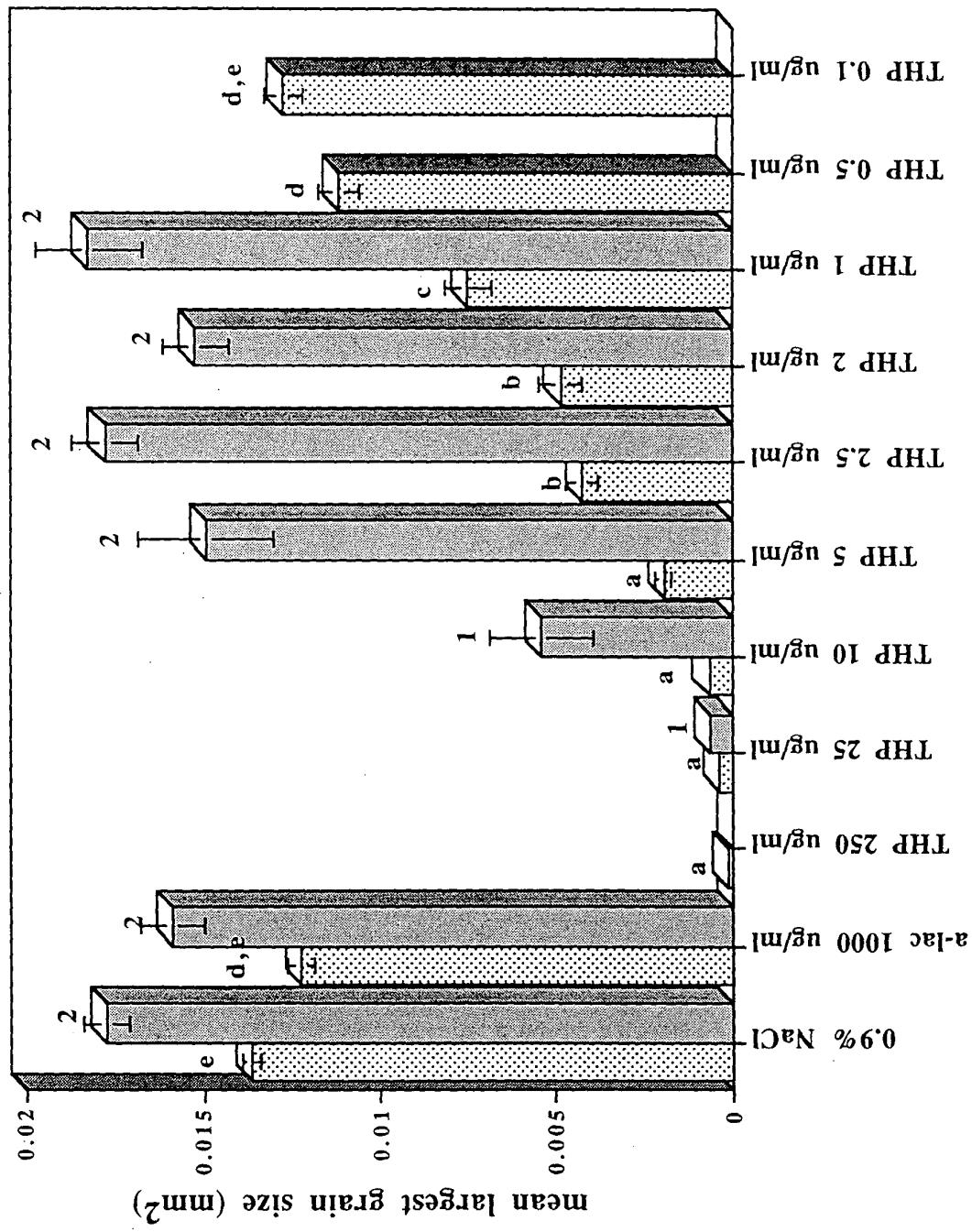


FIG. 8.15

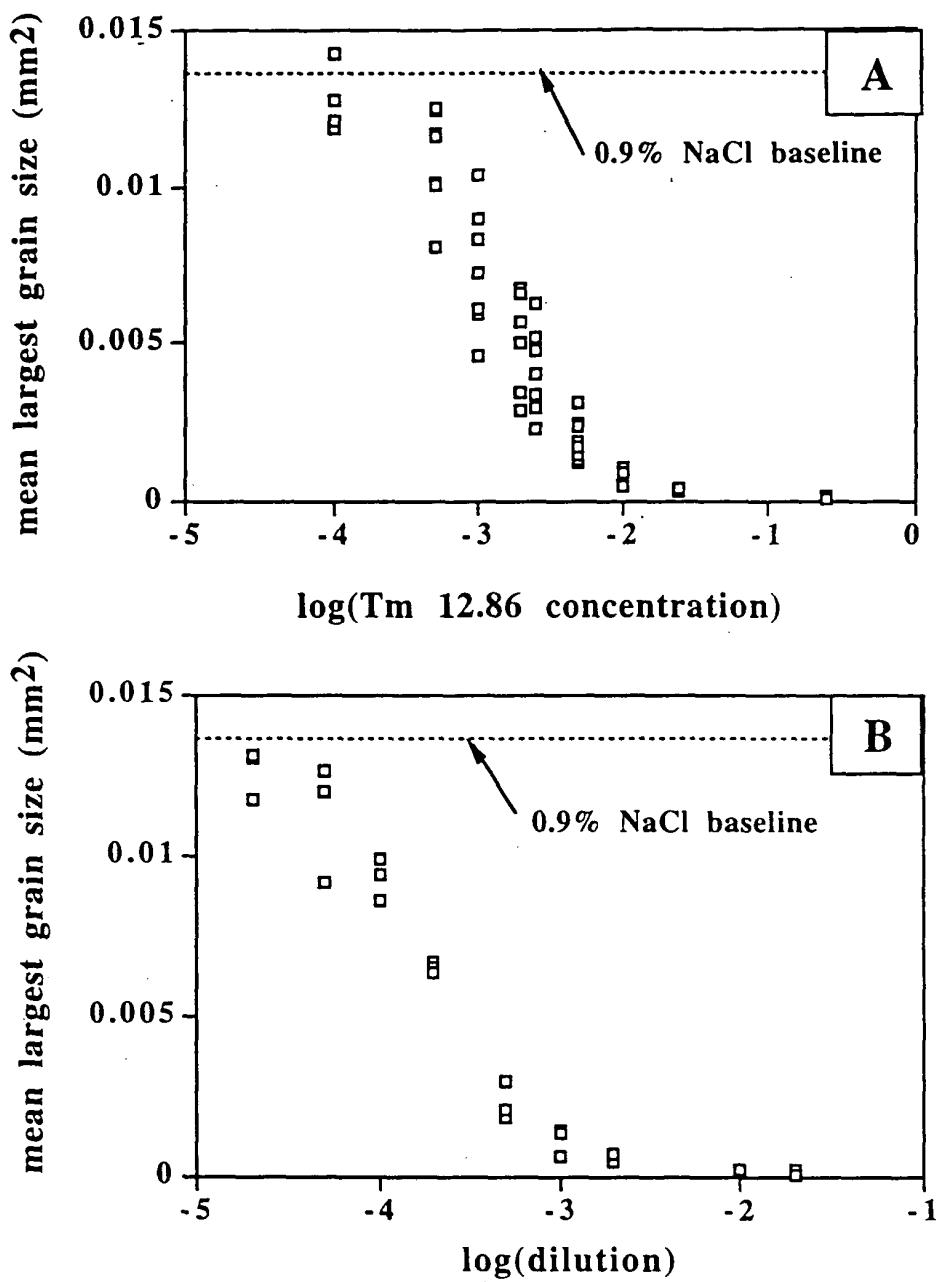


FIG. 8.16

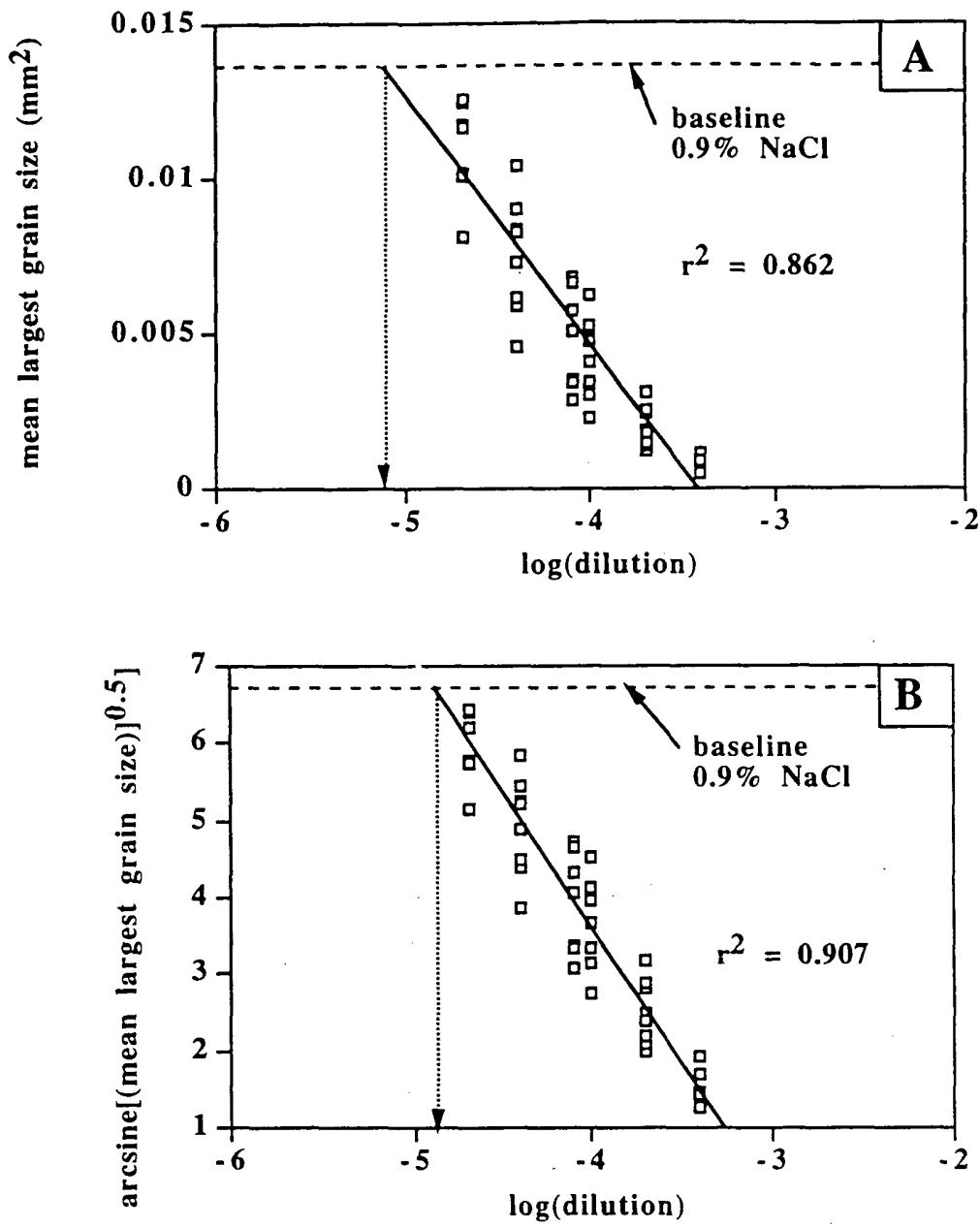


FIG. 8.17

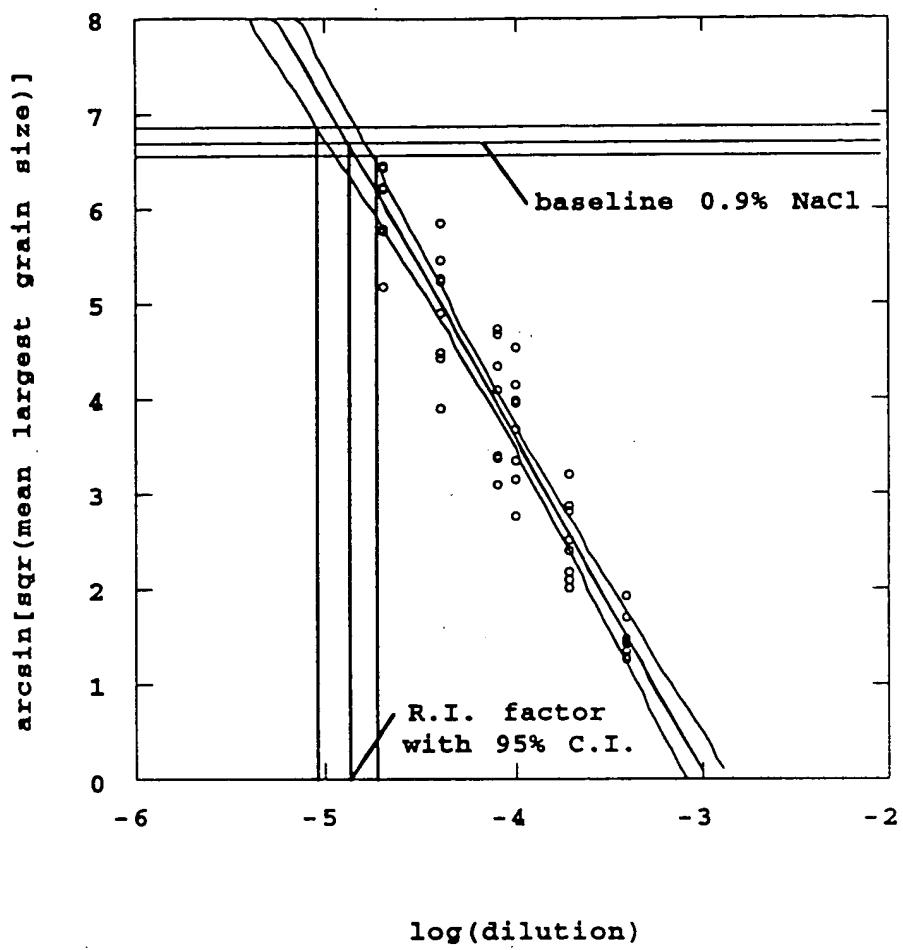


FIG. 8.18

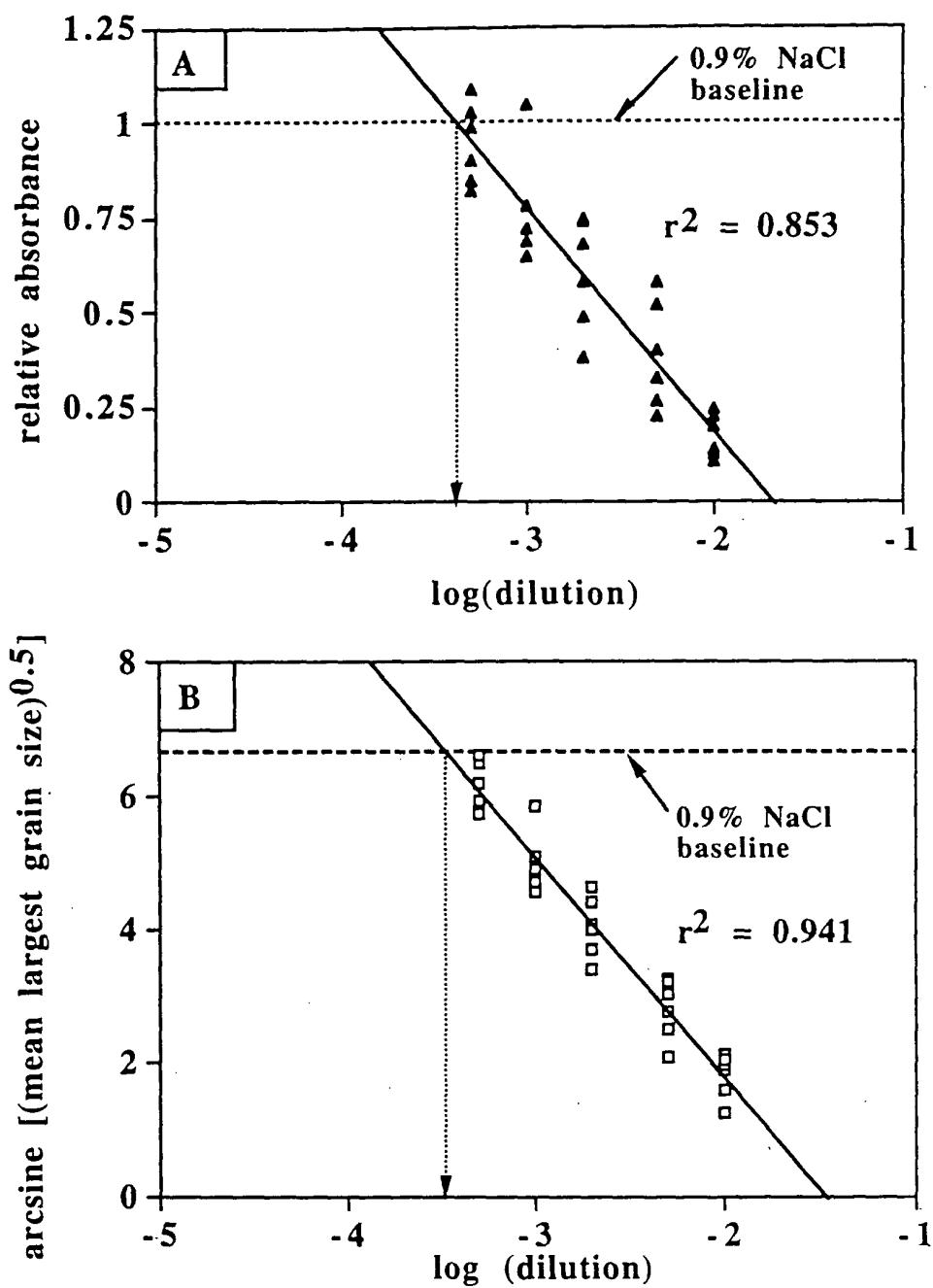


FIG. 8.19

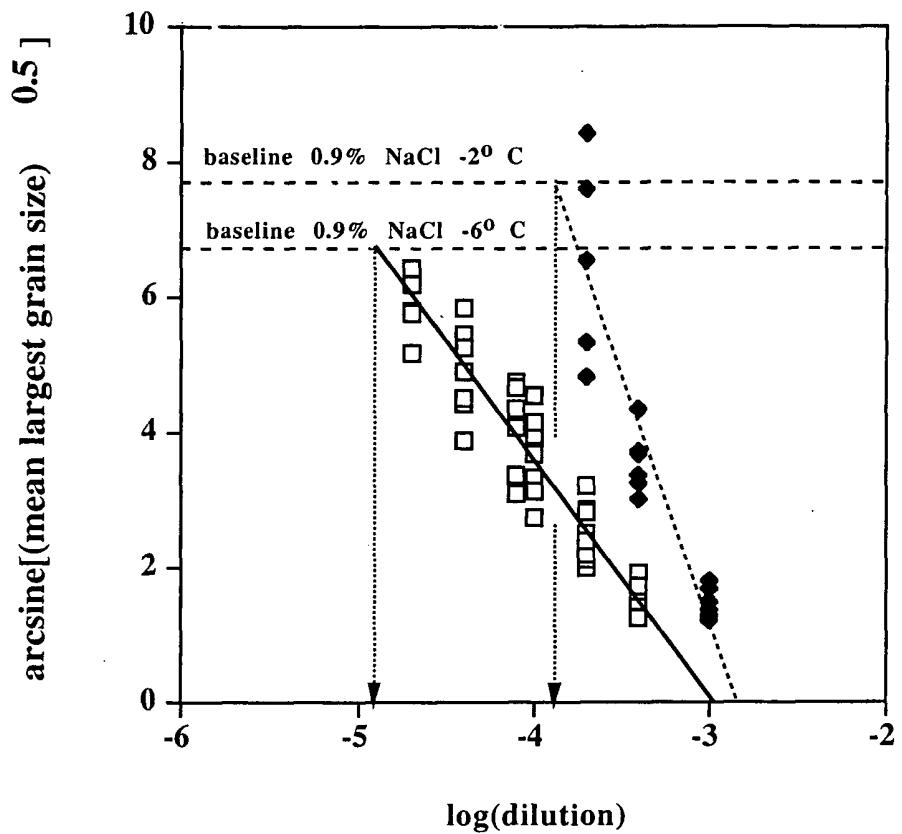


FIG. 8.20

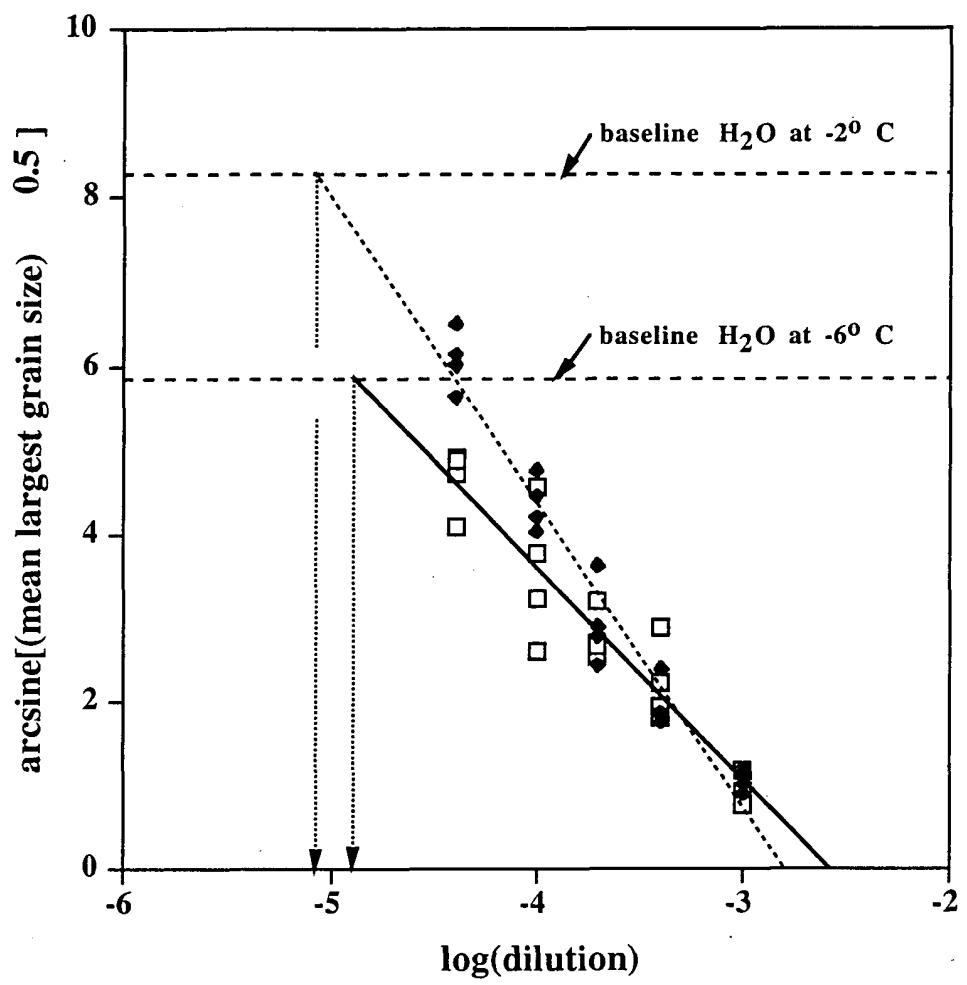


FIG. 8.21

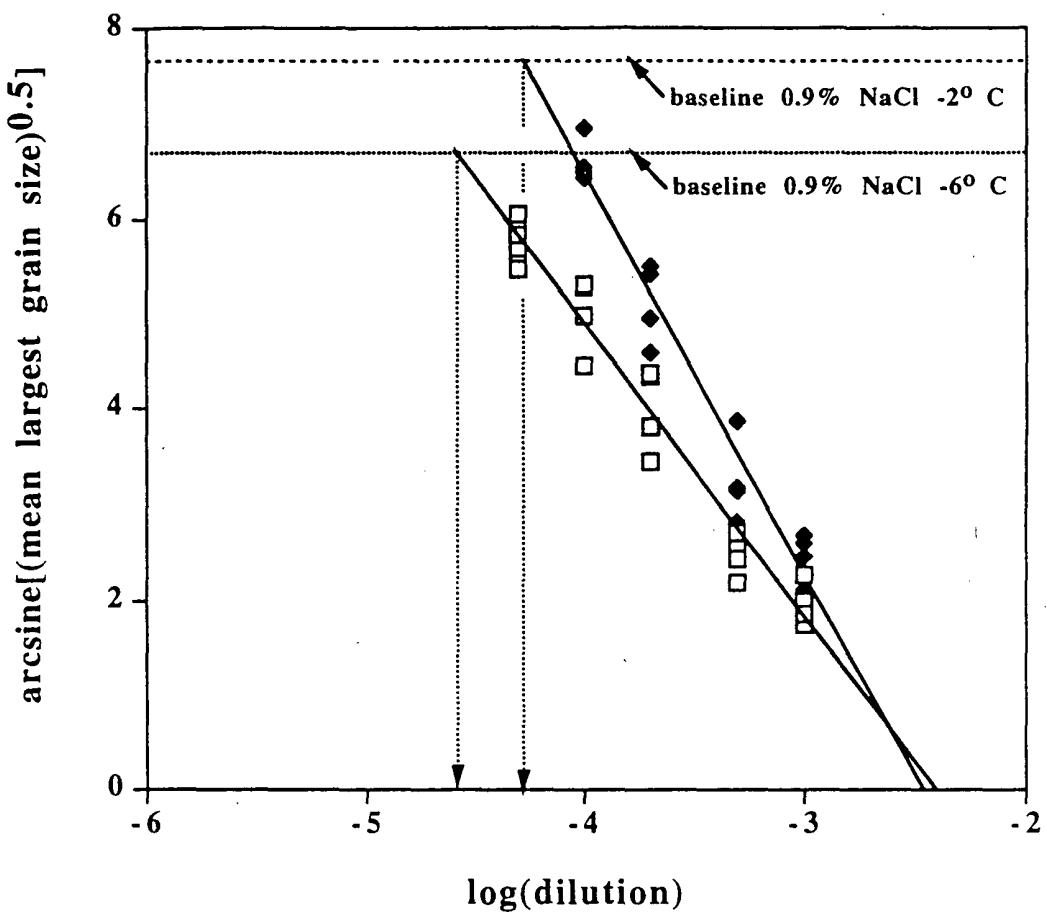


FIG. 8.22

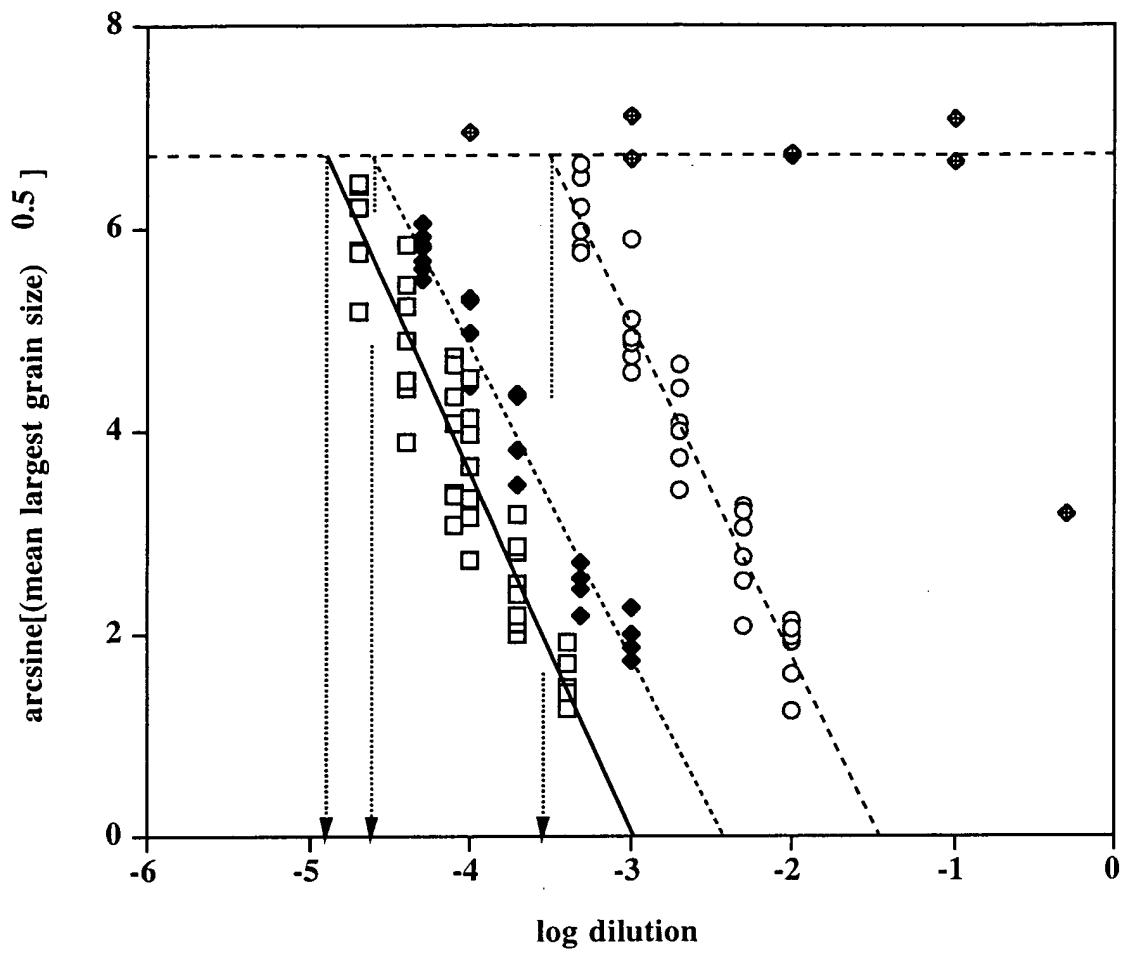
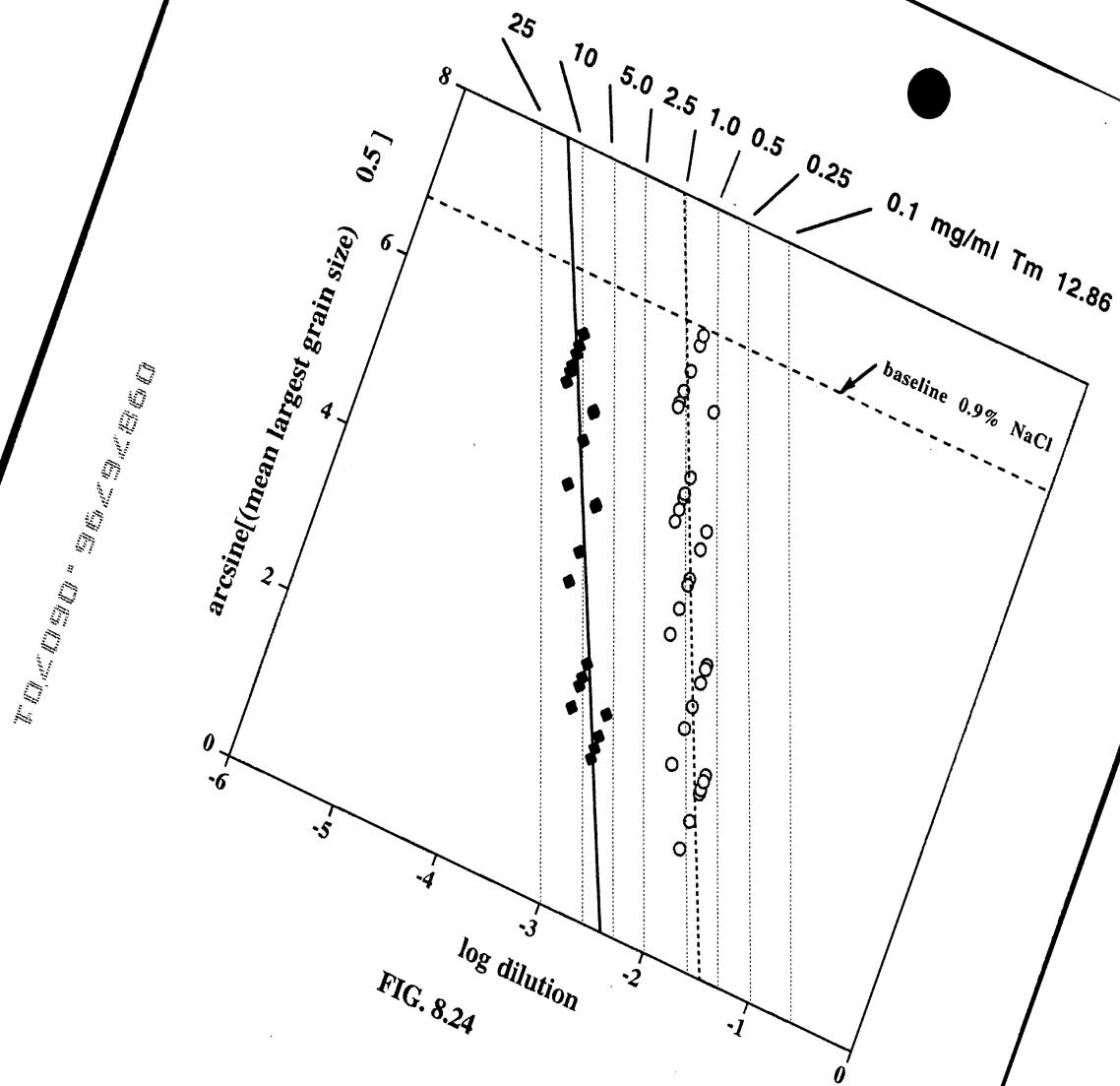


FIG. 8.23



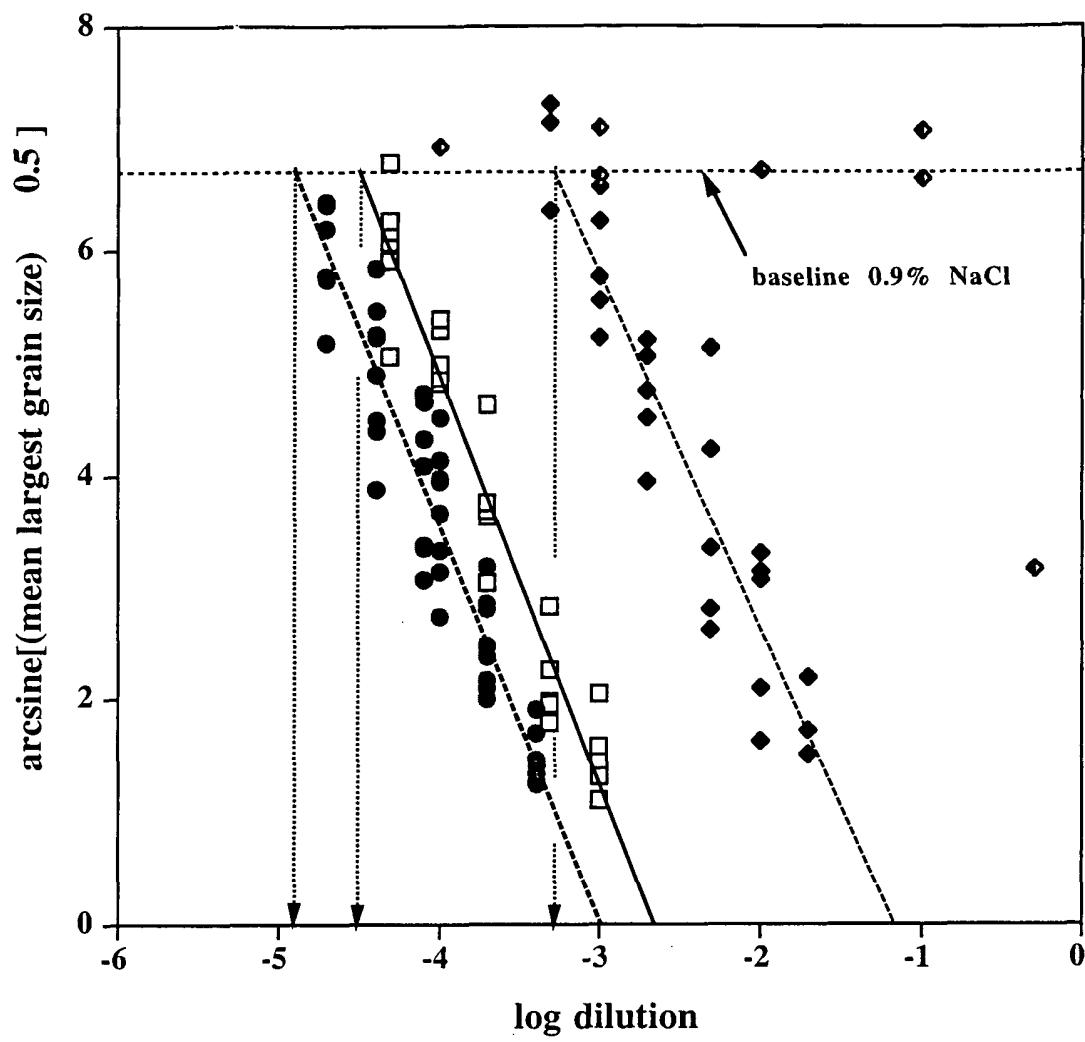
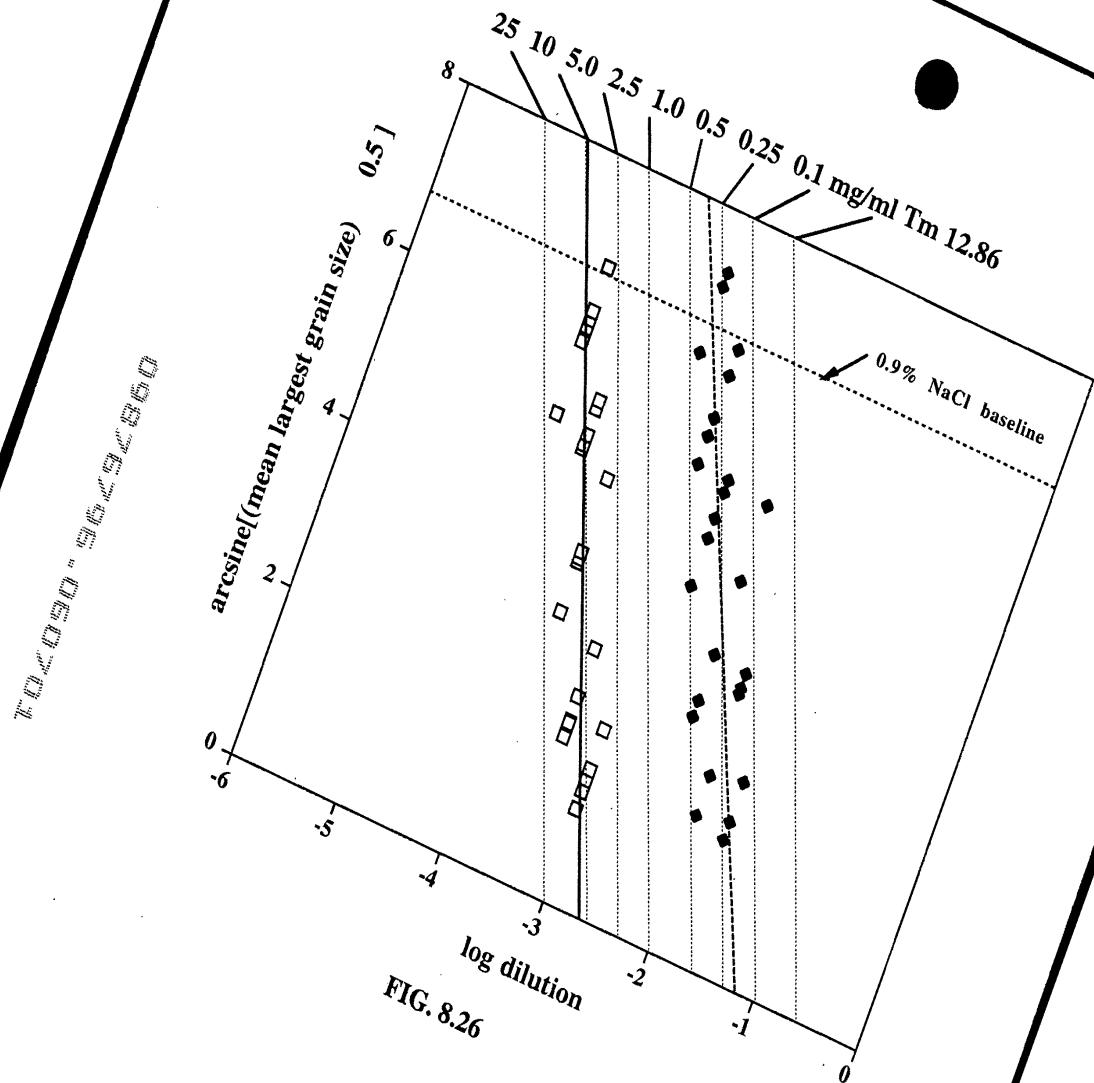


FIG. 8.25



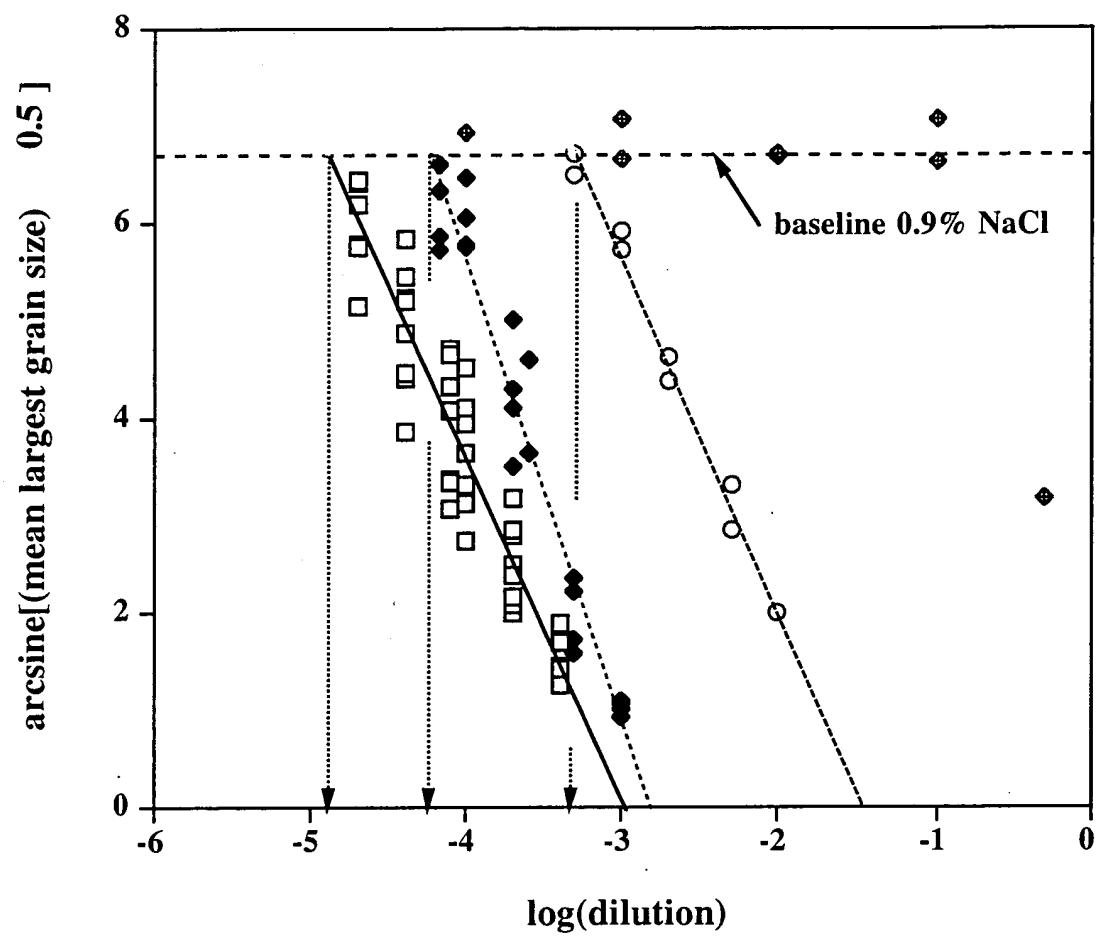


FIG. 8.27

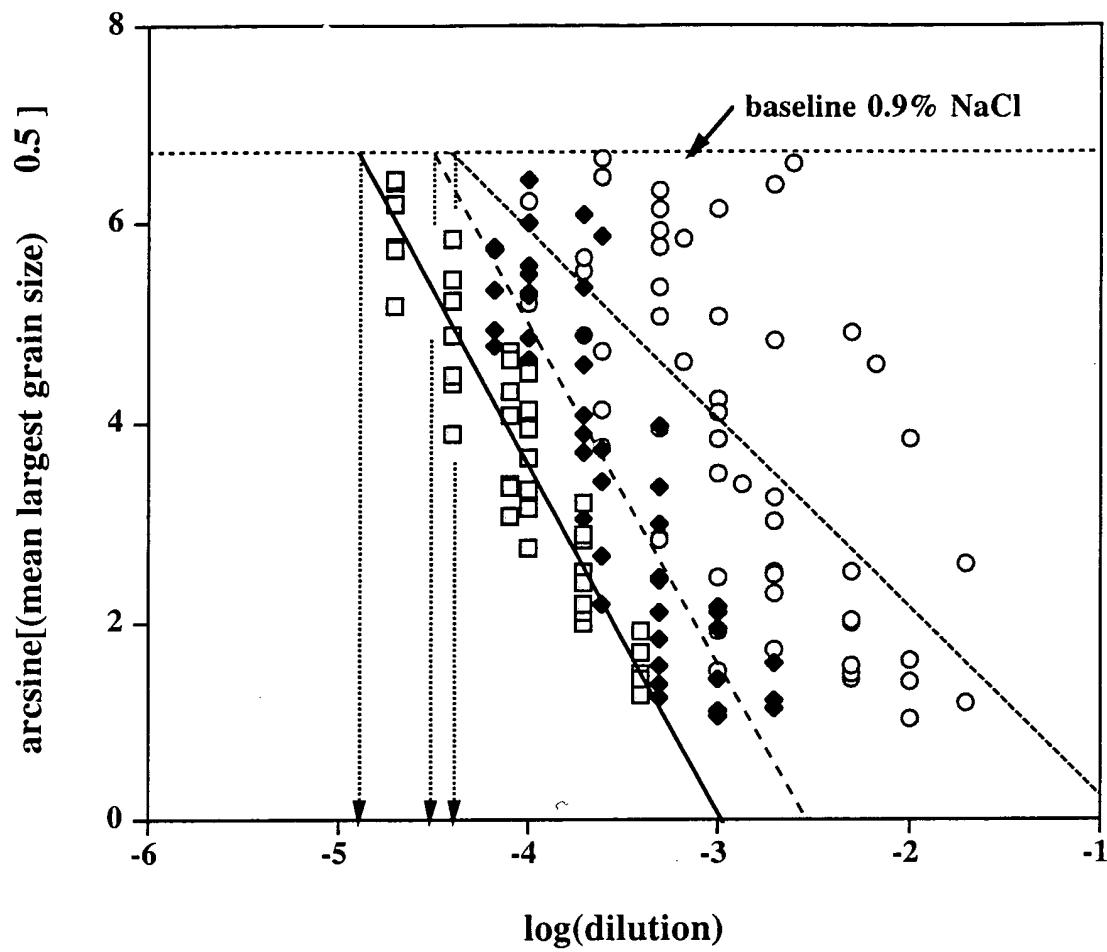


FIG. 8.28

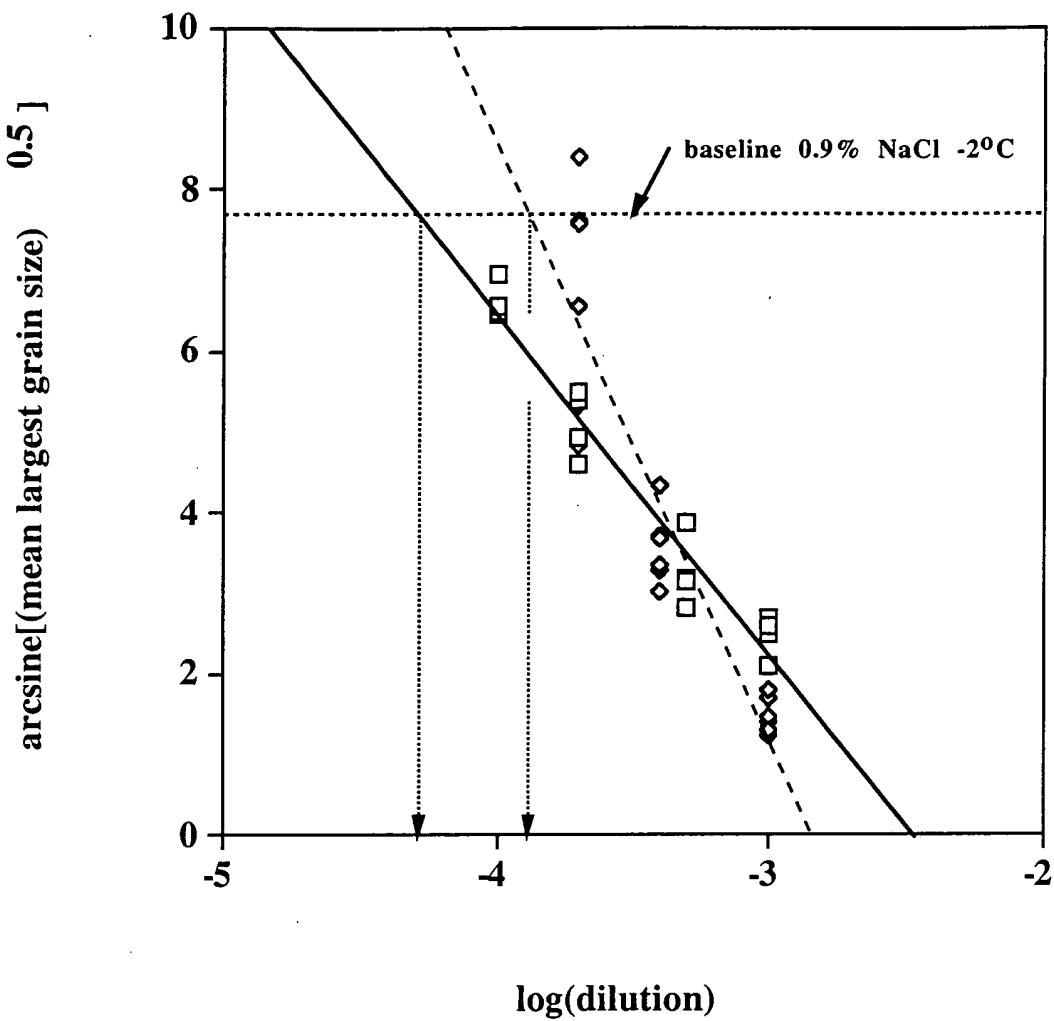


FIG. 8.29

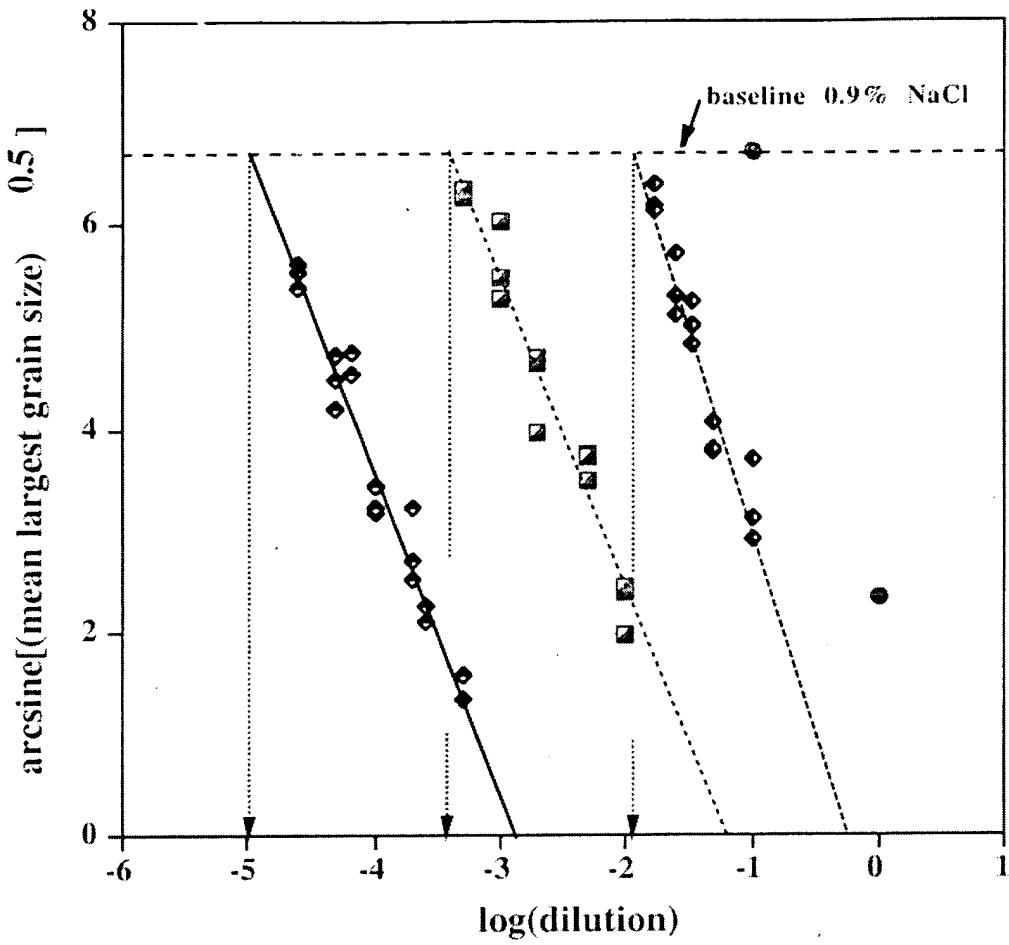


FIG. 8.30

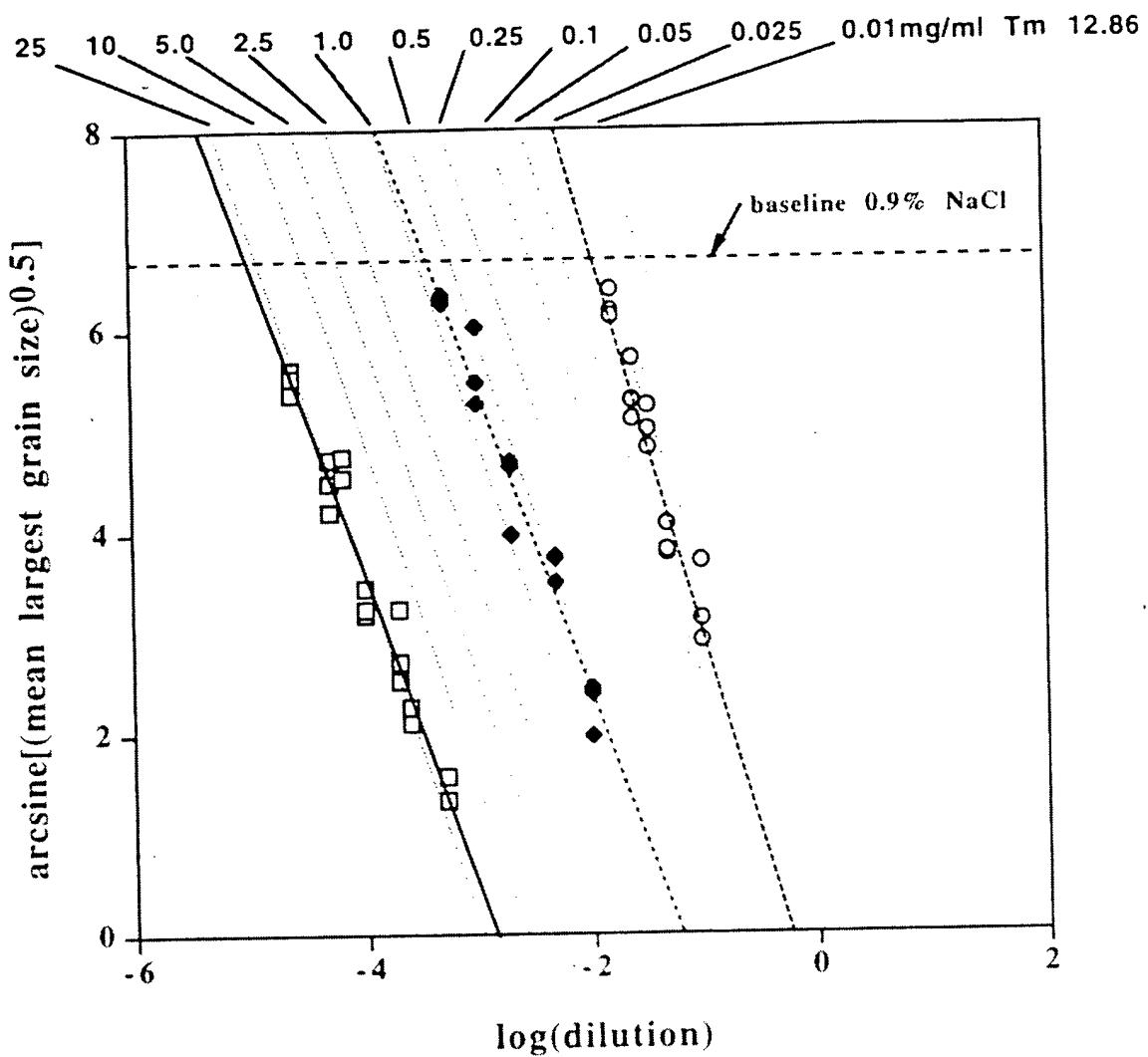


FIG. 8.31

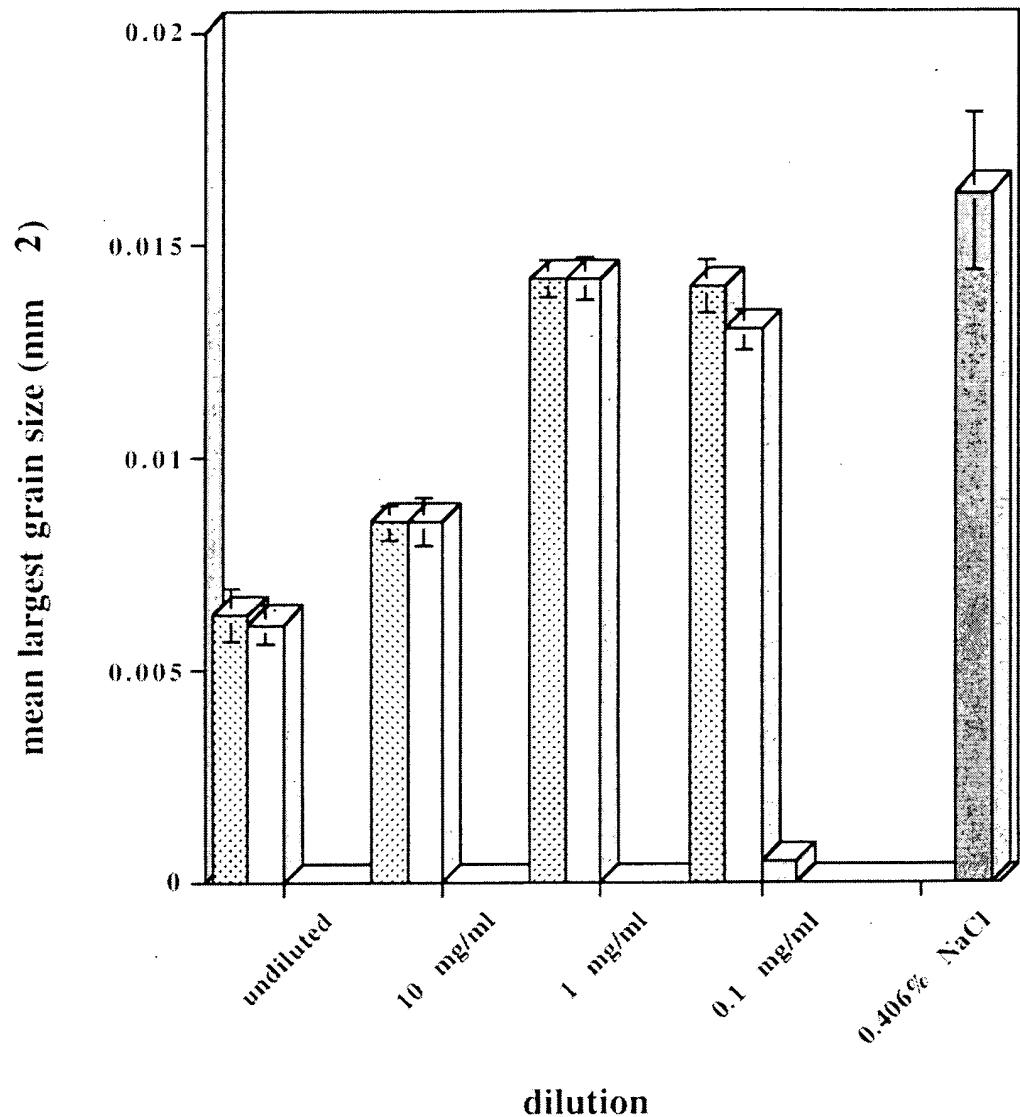


FIG. 8.32

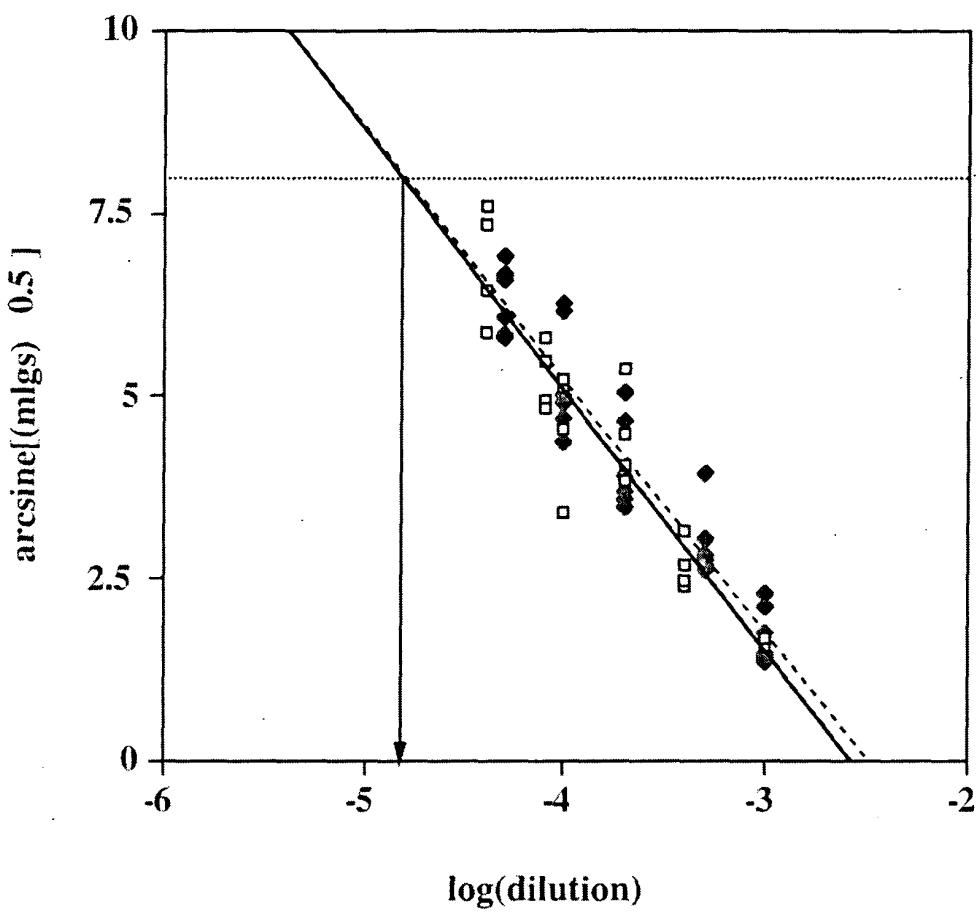


FIG. 8.33

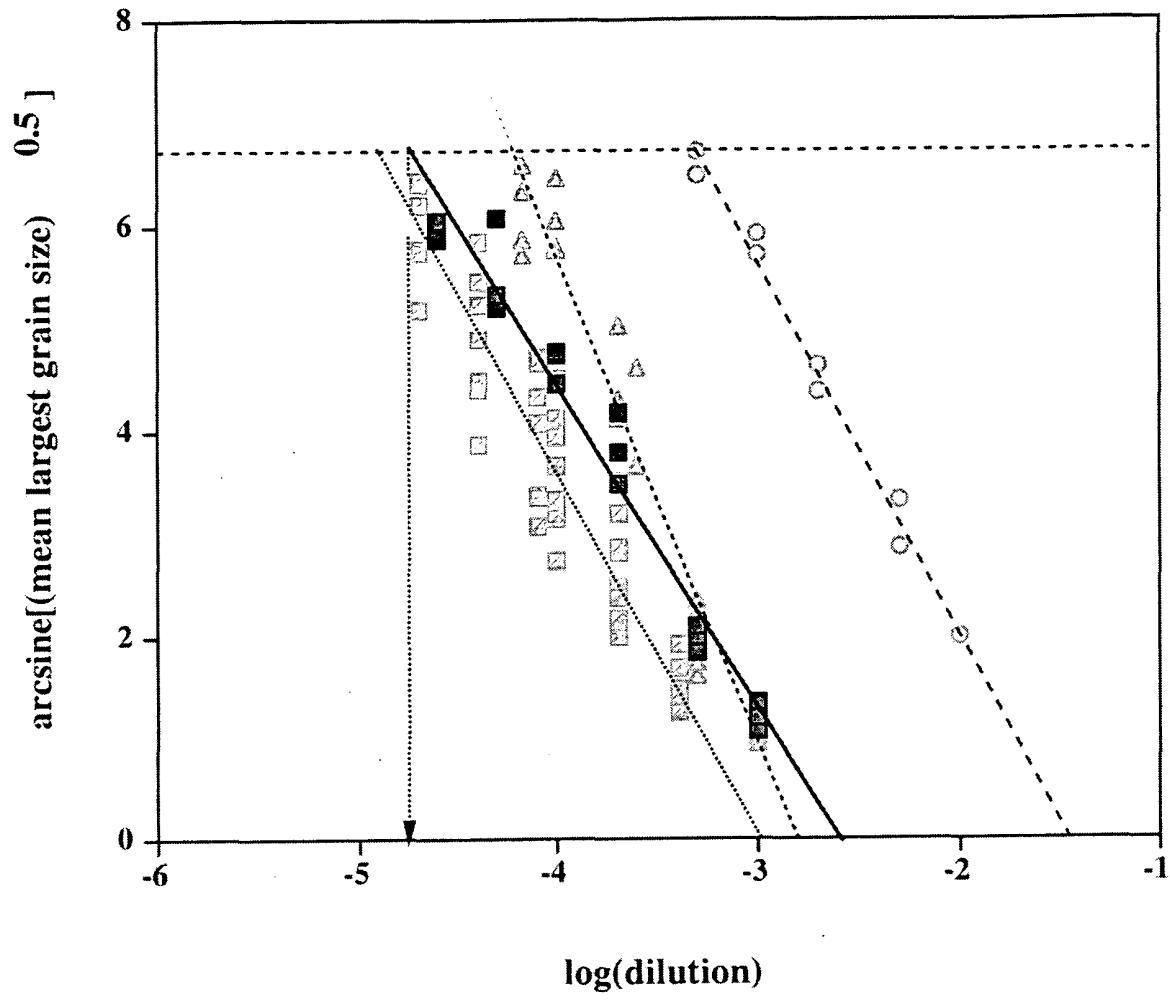


FIG. 8.34

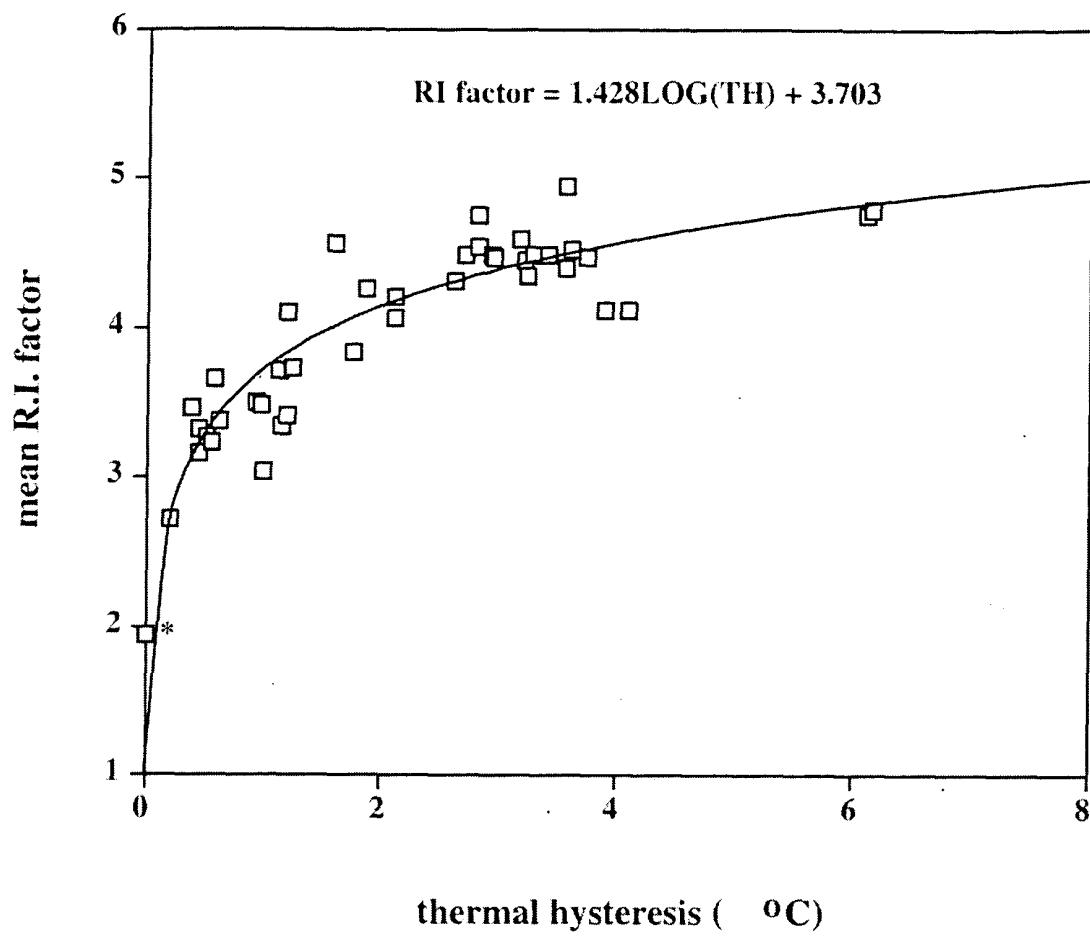


FIG. 8.35

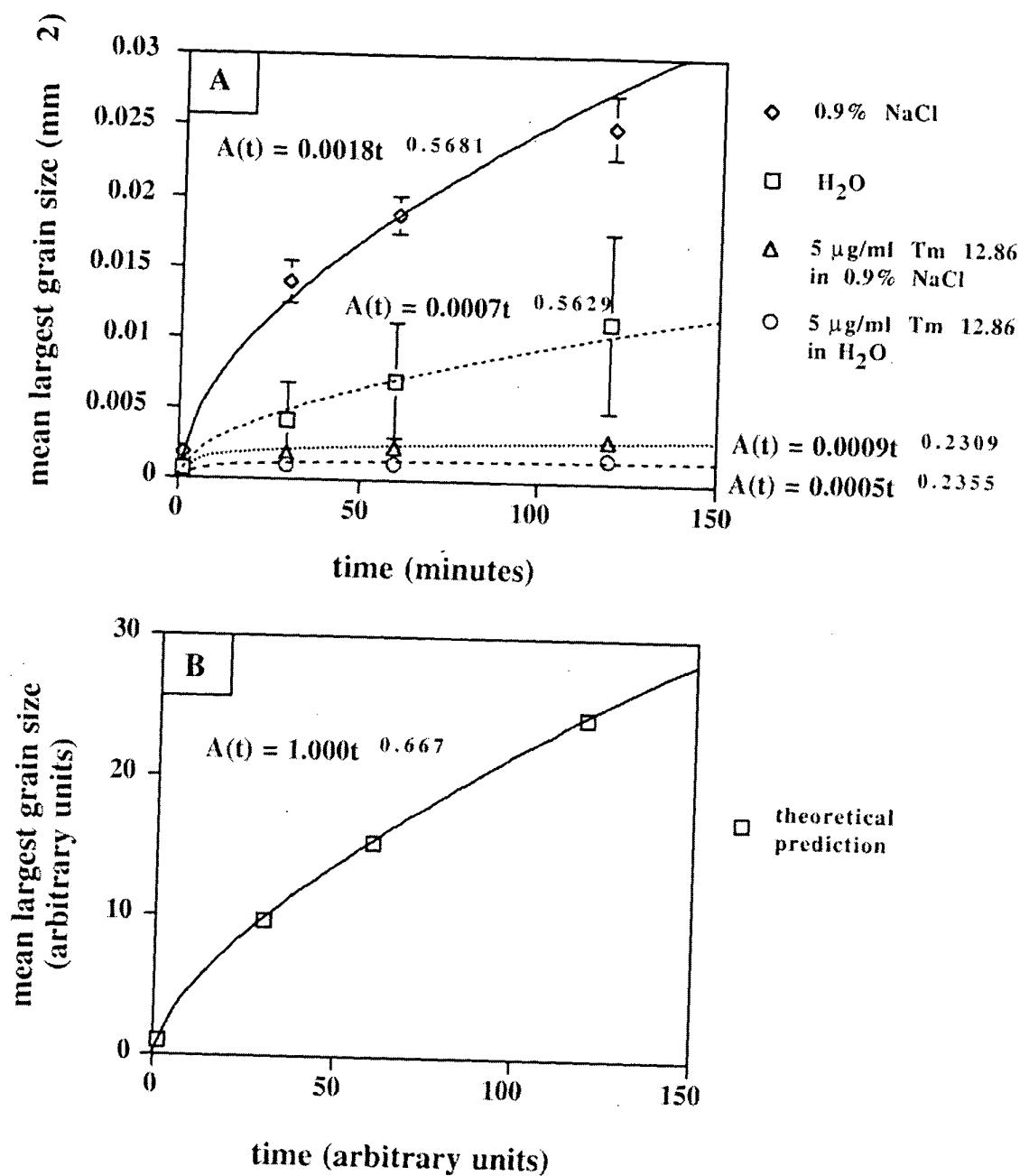


FIG. 8.36

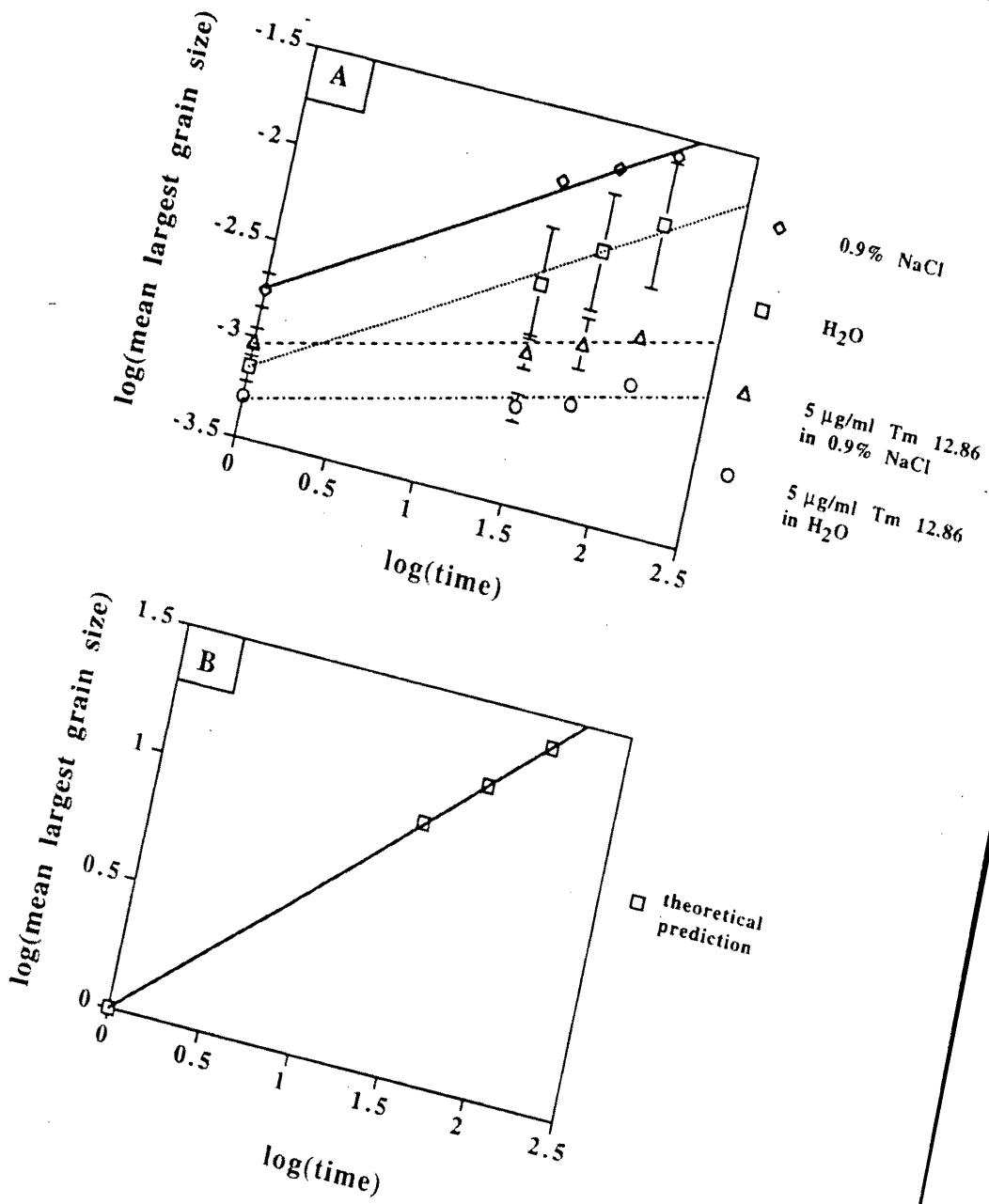
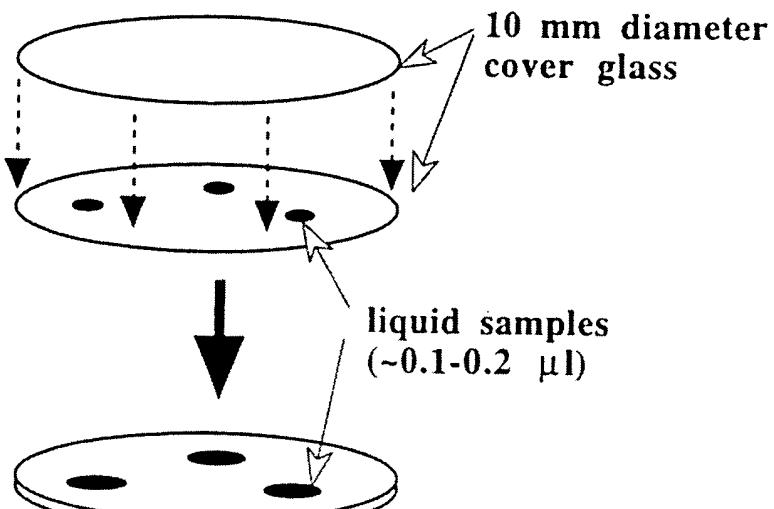


FIG. 8.37

"Sandwich" method of R.I. assessment

1.



2.

3. FREEZE ON ~-80 C
ALUMINUM PLATE (~10 MIN.)



4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS

FIG. 8.38

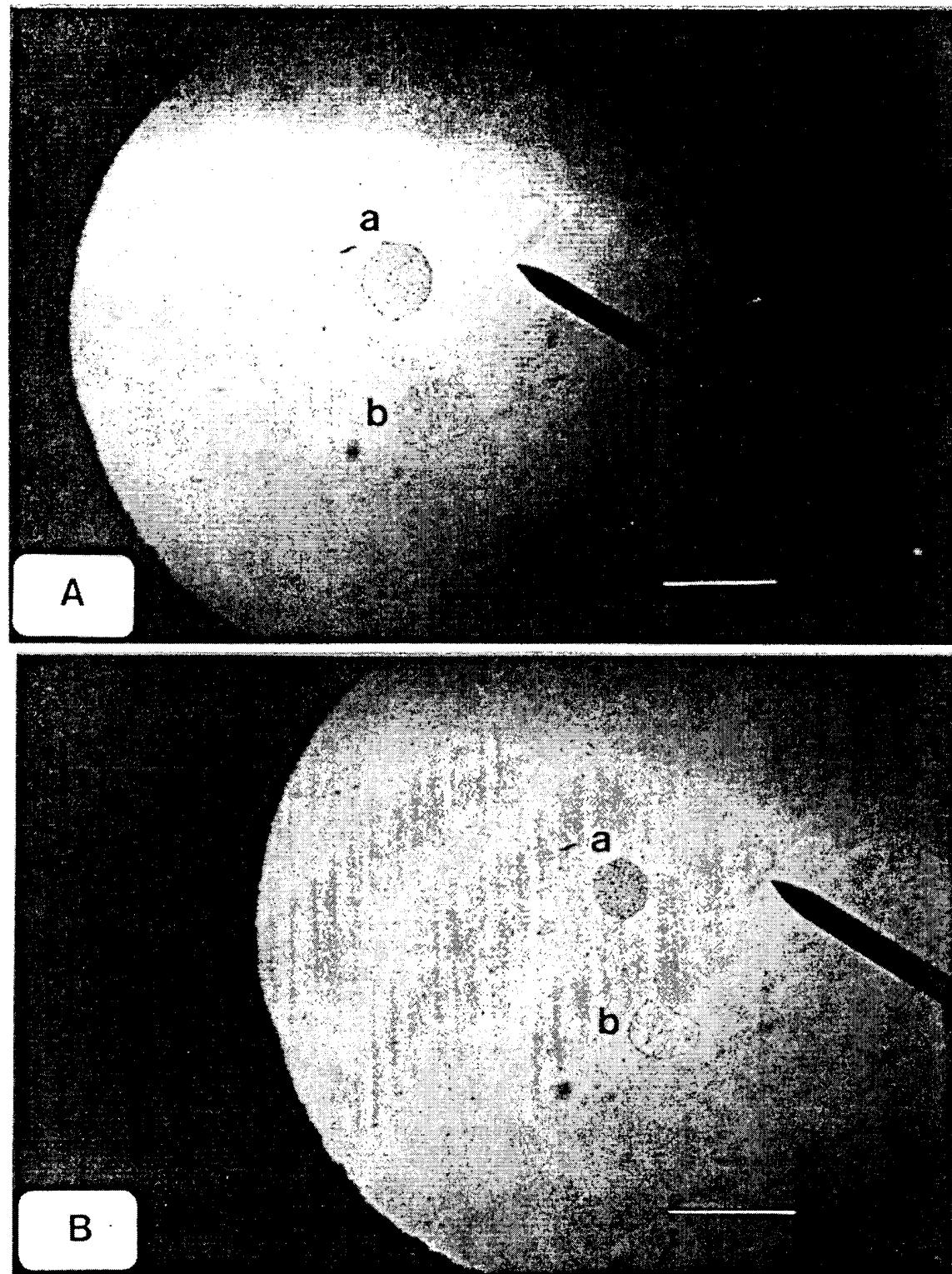


FIG. 8.39

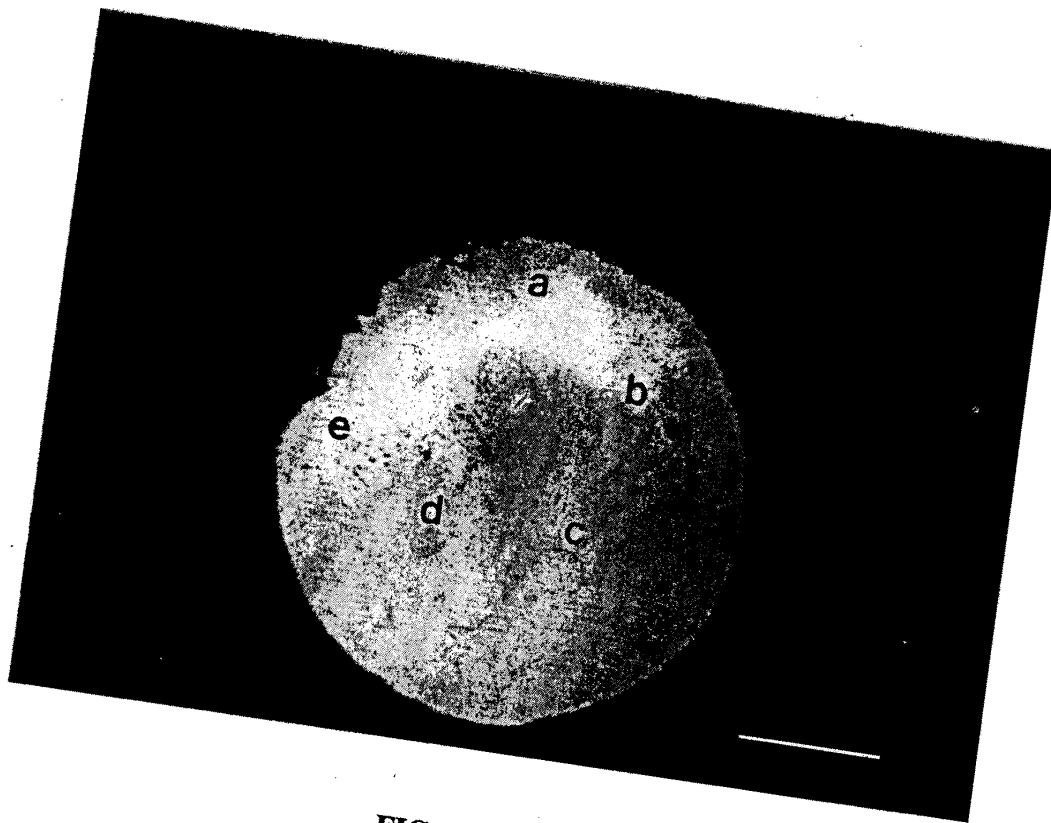


FIG. 8.40

09826296 - 06204

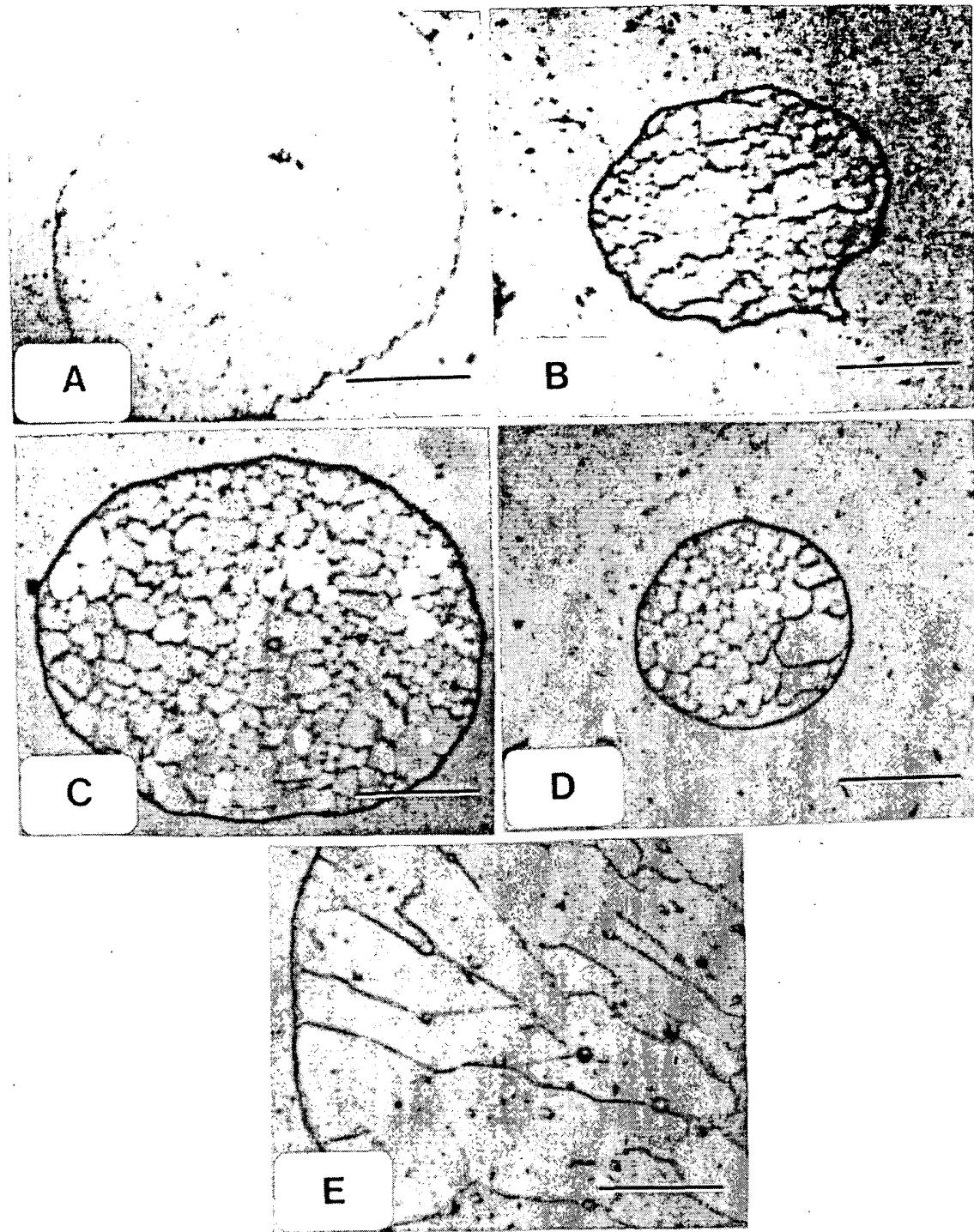


FIG. 8.41

09676296 - 060704

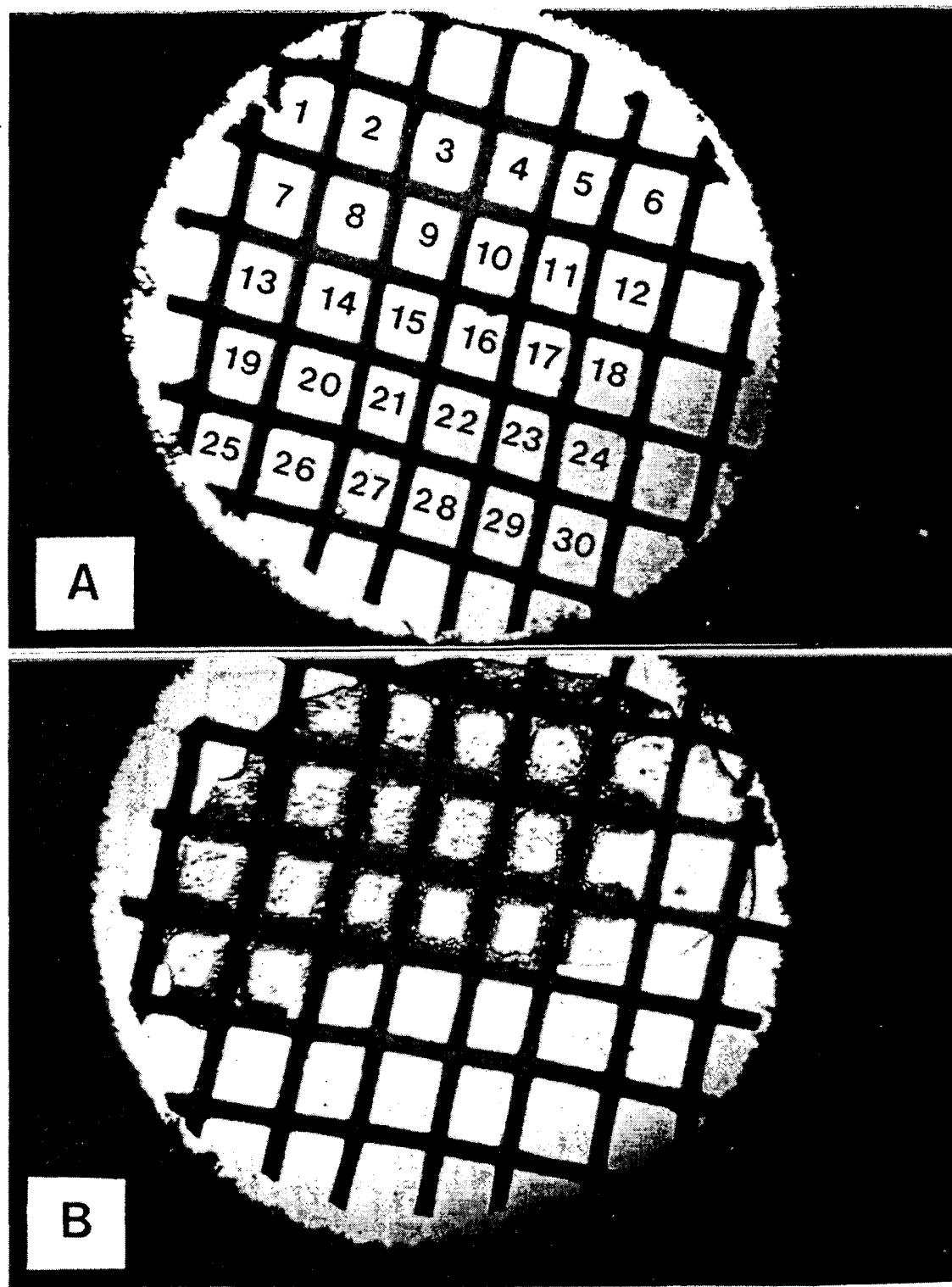


FIG. 8.42

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAACGATCAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTCAGGCCTGACCGAGGCACAAATTGAGAAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K ↑

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGAGATCATAACCAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGATCGGGAGAGGTGGTGGTCACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTCAATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAAGTGTGATTGAACCACCACGACTAGTAGATGGTCAAATGGTGTGCTTAC
F S P V D * X
h o i

481 ATATAAAAATAAAGTGTGTTCTGATGTAAAAAAAAAAAAAAAAAAACTC
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGCCATCGTTCCACCC

FIG. 8.43

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTGC GTT CGCCGCC
 M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA
 I V I G A Q A L T D E Q I Q K

92 AGGAACAAAGATCAGCAAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTGGTCGATGAT
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
 P K M K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V

316 CAGAAGTGC GTGGTCAAGAAGGCCACACCAAGAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTCTCTCC
 D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTGACAATAAGGT
 I D *

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAA

poly (A) tail

FIG. 8.44